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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

very Match 100.0%; Score 644; DB 9; Length 119;
est Local Similarity 100.0%; Pred. No. 4.4e-62;
atches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 RRKFTVSLGLPKQCPDHFHKGKVKTRHQRHKKPKNHSRACQQLKCOLRSFALPL 119

ULT 2
09-989-723-165
sequence 165, Application US/09989723
atent No. US2002007292A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.4e-62;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

US-09-989-279-165
 ; Sequence 165, Application US/09989279
 ; Patent No. US20020072496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC56
 ; CURRENT APPLICATION NUMBER: US/09/989,279
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
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 ; PRIOR FILING DATE: 1997-11-24

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Query Match 100.0%; Score 644; DB 9; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKVLSSLLLLPLMLMSWSSSLNPGVARGHRDRGQASRWLQGGQCECKDWFRLAP 60
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61 RRKFTVSLPKKQPCDHPKGNVKKTRHQRHKKPKHKSRAQQFLKQQLRSPALPL 119
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RESULT 4
3-09-989-727-165
Sequence 165, Application US/09989727
Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Aehkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
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APPLICANT: Goddard, Paul J.
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APPLICANT: Roy, Margaret Ann
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C65
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,727
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 9; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.4e-62;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHDEGQASRWLCEGGQCECKQWFLRAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHDEGQASRWLCEGGQCECKQWFLRAP 60
 QY 61 RRKFMTVSGLPKQPCDHFHKGKGVKXKTRHQRHHRKPNKXSRACQOFLKQCQLRSFALPL 119
 DB 61 RRKFMTVSGLPKQPCDHFHKGKGVKXKTRHQRHHRKPNKXSRACQOFLKQCQLRSFALPL 119

RESULT 5
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 ; Sequence 165, Application US/09989731
 ; Patent No. US20020103125A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deanevaya, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kijavini, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC70
 ; CURRENT APPLICATION NUMBER: US/09/989,731
 ; PRIOR FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-03-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28

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134 PRIOR FILING DATE: 1998-06-26
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137 PRIOR APPLICATION NUMBER: 60/091478
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146 PRIOR FILING DATE: 1998-07-02

PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.4e-62; Indels 0; Gaps 0;
 Matches 119; Conservative 0; Mismatches 0;
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 c 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRRWLQEGGQCECKDWFLRAP 60
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RESULT 6
 S-09-989-732-165
 Sequence 165, Application US/09989732
 Patent No. US20020123463A1
 GENERAL INFORMATION:

APPLICANT: Ashtenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zenin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC57
 CURRENT APPLICATION NUMBER: US/09/989,732

PRIOR FILING DATE: 2001-11-19
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 ;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.4e-62;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDGGASRRWLQGGQCECKDWFLRAP 60
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 DB 61 RRKFTVSGLPKKQCPCHDFKGNVKTQRHRRKPKNKHGRACQOFLKQQLRSFALPL 119

RESULT 7

US-09-991-073-165
 ; Sequence 165, Application US/09991073
 ; Patent No. US20020127576A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC15
 ; CURRENT APPLICATION NUMBER: US/09/991,073
 ; CURRENT FILING DATE: 2001-11-14
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74	PRIOR APPLICATION NUMBER: 60/091982	
75	PRIOR FILING DATE: 1998-07-07	
76	PRIOR APPLICATION NUMBER: 60/092182	
77	PRIOR FILING DATE: 1998-07-09	

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Query Match      100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred.No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKVLISLLLLPLMLSMVSSSSLNPGVARGHRDRGQASRRWLQEGGQCECKQDFLRAP 60

2Y 61 RRKEMTVSGLPKQPCDHPKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL 119
DB 61 RRKEMTVSGLPKQPCDHPKGNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL 119

RESULT 8
JS-09-990-442-165
Sequence 165, Application US/09990442
Patent No. US2002013252A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT APPLICATION NUMBER: US/09/990,442
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-07-09

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Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9

US-09-991-163-165
; Sequence 165, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC17
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 / PRIOR FILING DATE: 1998-07-07
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 / PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
 Best Local Similarity 100.0%; Pred. No. 4.4e-62;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10

S-09-993-604-165

Sequence 165, Application US/09993604

Patent No. US20020137075A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

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APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C25

CURRENT APPLICATION NUMBER: US/09/993,604

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

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PRIOR FILING DATE: 1997-11-24

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PRIOR FILING DATE: 1998-02-25

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62 PRIOR FILING DATE: 1998-07-07
63 PRIOR APPLICATION NUMBER: 60/092182
64 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKVLISLILLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFILRAP 60

Cy 61 RRKFTVSGIPKKQCPCHFKGNVKKTRHQRHRRKPKHKSACQFLKQCOLRSGFALPL 119
Db 61 RRKFTVSGIPKKQCPCHFKGNVKKTRHQRHRRKPKHKSACQFLKQCOLRSGFALPL 119
RESULT 11
US-09-990-456-165
Sequence 165, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1G22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDQASRRWLQEGQCECKDWFLRAP 60
Db 1 MKVLISLLLLPLMLSMVSSSLNPGVARGHRRDQASRRWLQEGQCECKDWFLRAP 60
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Db 61 RRKFTVSGLPKXQPCDHFPGNVKKTROHRRKPKNSRACQFLKQCLRSFALPL 119

RESULT 12
US-09-989-721-165
Sequence 165, Application US/0989721
Patent No. US2002042961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC55
CURRENT APPLICATION NUMBER: US/09/989,721
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;; PRIOR APPLICATION NUMBER: 60/091982
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKVITSSLLLLPLMLMSVSSSLNPGVARGHRRDQASRRWLQEGQCECKDWFLRAP 60
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DB 61 RKMTVSGLPKKQPCDHFKNVKTTRHORHRRKNKHSRACQQLKQCLASFALPL 119

RESULT 14
US-09-989-293A-165
; Sequence 165. Application US/09989293A
; Patent No. US20020177164A1

GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnovers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730P1C66
 CURRENT APPLICATION NUMBER: US/09/989,293A
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;

Best Local Similarity 100.0%; Pred. No. 4.4e-62;

Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RRKFMVTSGLPKKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCLRSFALPL 119

RESULT 15

US-09-389-735-165

; Sequence 165, Application US/09989735

; Publication No. US20020193299A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C61
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CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 10; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLEAP 60
Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLEAP 60
Qy 61 RRKFMVTVSGLPKKQCPDHFKNVKTTHQRHHRKPNKHSRACQOFLKQCOLRSEFALPL 119
Db 61 RRKFMVTVSGLPKKQCPDHFKNVKTTHQRHHRKPNKHSRACQOFLKQCOLRSEFALPL 119

Search completed: January 29, 2004, 11:57:31
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 11:53:38 ; Search time 21 Seconds
(without alignments)
239.762 Million cell updates/sec

Title: US-09-786-260-1
Perfect score: 644
Sequence: 1 MKVLISLLILLPLMLSMV.....SRACQFLKQCLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5E_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	119	4	US-09-996-243-165
2	84.5	13.1	620	4	US-09-252-991A-17301
3	74	11.5	629	4	US-09-252-991A-16777
4	73.5	11.4	70	1	US-07-737-736B-3
5	72.5	11.3	724	4	US-09-252-991A-28517
6	72	11.2	689	4	US-09-252-991A-19258
7	70.5	10.9	420	4	US-09-252-991A-27610
8	70	10.9	188	1	US-08-469-427A-11
9	70	10.9	188	2	US-08-609-443B-11
10	70	10.9	188	2	US-08-569-063C-11
11	70	10.9	188	3	US-08-795-430-57
12	70	10.9	188	4	US-08-851-896-11
13	70	10.9	188	4	US-09-355-700-57
14	70	10.9	188	4	US-09-431-888-6
15	70	10.9	626	4	US-09-252-991A-30510
16	69.5	10.8	446	1	US-08-307-444A-5
17	69.5	10.8	446	1	US-08-587-389-5
18	69.5	10.8	456	1	US-08-307-444A-3
19	69.5	10.8	456	1	US-08-307-444A-4
20	69.5	10.8	456	1	US-08-587-389-3
21	69.5	10.8	456	1	US-08-587-389-4
22	69.5	10.8	475	1	US-08-307-444A-1
23	69.5	10.8	475	1	US-08-307-444A-2
24	69.5	10.8	475	1	US-08-587-389-1
25	69.5	10.8	475	1	US-08-587-389-2
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27	69.5	10.8	476	1	US-08-014-723-2

Sequence 18, Appl
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Sequence 4, Appl
Sequence 2, Appl
Sequence 27039, A
Sequence 59, Appl
Sequence 1, Appl
Sequence 54, Appl
Patent No. 5466668
Sequence 24867, A
Sequence 21486, A

ALIGNMENTS

RESULT 1
US-09-996-243-165
; Sequence 165, Application US/09996243
; Patent No. 6478825
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, F. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC13
; CURRENT APPLICATION NUMBER: US/09/996,243
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28

PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801	PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908	PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23	PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633

PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 644; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 4.1e-69;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLILLLPLMLMSVSSSLNPGVGHDRDGOASRWLQEGGQCECKDWFLRAP 60
DB 1 MKVLISLILLLPLMLMSVSSSLNPGVGHDRDGOASRWLQEGGQCECKDWFLRAP 60
QY 61 RKKFTVSGLPKQCPDHFKNVKTTHORHHRKPKNSRACQFLKQCQLRSFALPL 119
DB 61 RKKFTVSGLPKQCPDHFKNVKTTHORHHRKPKNSRACQFLKQCQLRSFALPL 119

RESULT 2

US-09-252-991A-17301
Sequence 17301, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17301
LENGTH: 620
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17301

Query Match 13.1%; Score 84.5; DB 4; Length 620;
Best Local Similarity 30.7%; Pred. No. 0.099;
Matches 27; Conservative 11; Mismatches 23; Indels 27; Gaps 4;

QY 29 ARGHRDRGQA-----SRRLQEGGQCECKDWFLRAPRKFTVSGLPKQCPDHFKN 83
DB 538 ASHRDRGQQRDHNRHRRPHREGRCQRE--DQVRRPHR-----GR 576
QY 84 VKKTRHQRHHRKPKNSRACQFLKQCQ 111
DB 577 RQQRDHQ-HRRRPHREGRCQQRDQHRQ 603

RESULT 3

US-09-252-991A-16777
Sequence 16777, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16777
LENGTH: 629

TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16777

Query Match 11.5%; Score 74; DB 4; Length 629;
Best Local Similarity 30.2%; Pred. No. 1.8;
Matches 32; Conservative 10; Mismatches 28; Indels 36; Gaps 7;

QY 24 LNPVG-----ARGHRDRGQASRR-----WLQGGQCECKDWFLRAPRKFTVSGLPK 72
DB 448 VRPGDLLRLRRHRLRQGRHRLRLQWLRTGG-----RDPRR---SVARLFR 494
QY 73 KQCPDHFKNVKTTHORHHRKPKNSRACQFLKQCQLRSFALP 118
DB 495 -----HLHG-----VHRLHRRSPDRH-RGAPPALSQPARRTGKP 528

RESULT 4

US-07-737-736B-3
Sequence 3, Application US/077377736B
Patent No. 5260199

GENERAL INFORMATION:

APPLICANT: Deluca, Hector F.
APPLICANT: Ross, Troy K.
APPLICANT: Prah, Jean M.
TITLE OF INVENTION: Method Of Producing
TITLE OF INVENTION: 1,25-Dihydroxyvitamin D3 Receptor Protein
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Carl E. Schwartz, Esq., c/o Quarles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,736B
FILING DATE: 19910730
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Carl E.
REGISTRATION NUMBER: 29,437
REFERENCE/DOCKET NUMBER: 96-296-2185-2
TELEPHONE: 414-277-5715
TELEFAX: 414-277-5774
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Chicken
PUBLICATION INFORMATION:
AUTHORS: McDonnell, Donald P.
AUTHORS: Mangelsdorf, David J.
AUTHORS: Pike, J. W.
AUTHORS: Haussler, Mark R.
AUTHORS: O'Malley, Bert W.
TITLE: Molecular Cloning of Complementary DNA
JOURNAL: Science
VOLUME: 235
PAGES: 1214-1217

DATE: March 6-1987

US-07-737-736B-3

Query Match 11.4%; Score 73.5; DB 1; Length 70;
Best Local Similarity 35.5%; Pred. No. 0.14; 12; Indels 19; Gaps 5;
Matches 22; Conservative 9; Mismatches 31; Indels 17; Gaps 4;
QY 50 CE-CKWFLRPRKMTVSGLPKQPCDHFHKGNNVKTTHQHRHKKPKNSRACQFLK 108
DB 20 CEGCKGFFRSMKMKAMFT-----CP-----FNGDCKITKDNK-----RHQCAQR--LK 61

QY 109 QC 110
DB 62 RC 63

RESULT 5
US-09-252-991A-28517
; Sequence 28517, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28517
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28517

Query Match 11.3%; Score 72.5; DB 4; Length 724;
Best Local Similarity 28.4%; Pred. No. 3.2;
Matches 23; Conservative 10; Mismatches 31; Indels 17; Gaps 4;
QY 31 GHRDGRQASRWLQGGQCECKDWFRLAPRRKFTVSGLPKQPCDHFHKGNNVKTTHQ 90
DB 104 GRRDAGEAARR-RSGDPRDLREVLRL--RLRADRPQSPFPPSPGDAAGH---RHR 156
QY 91 RH-----HKKNKHSR 101
DB 157 HHPDRRQPDQGRHRRPRRSR 177

RESULT 6
US-09-252-991A-19258
; Sequence 19258, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19258
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19258

Query Match 11.2%; Score 72; DB 4; Length 689;
Best Local Similarity 40.5%; Pred. No. 3.5;
Matches 15; Conservative 5; Mismatches 15; Indels 2; Gaps 1;

QY 70 LPKQCC--PCDHFHKGNNVKTTHQHRHKKPKNSRACQ 104
DB 265 LGRROCLLPADLPQFQPELRRHRRHQRPRRTDRAVQ 301

RESULT 7

US-09-252-991A-27610
; Sequence 27610, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27610
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (367)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-27610

Query Match 10.9%; Score 70.5; DB 4; Length 420;
Best Local Similarity 24.8%; Pred. No. 2.9;
Matches 26; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 22 SSLNPGVAGHRDRGQASRRWLQGGQCECKDWFRLAPRRKFTVSGLPKQPCDHFH 81
DB 69 SSAQPLPGTGHQGGQSGRK--RHGQSVME-----HRQAITAVG--PQGPLRIEHN 116
QY 82 G-----NVKTRHQHRHKKPKNSRACQFLKQCOLRS 114
DB 117 GEFAGTARILEQRAEADAQDRHLLR-QRHHRPCRPVPPQCORRS 150

RESULT 8

US-08-469-427A-11
; Sequence 11, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: Eriksson, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Alitalo, Kari
; APPLICANT: Pajusela, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A

FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP2
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 TISSUE TYPE: human fibrosarcoma
 US-08-469-427A-11

Query Match 10.9%; Score 70; DB 1; Length 188;
 Best Local Similarity 28.4%; Pred. No. 1.2;
 Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

QY 43 LOEGGQCECKDWFLRAPRRKMTVS-GLPKQCPDHFKNVKKTRHQRHRRKPKHRSR 101
 DB 116 LEEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157

QY 102 ACQQLKQCOLRSP 115
 DB 158 RC-----RCRRRSF 166

RESULT 9
 US-08-609-443B-11
 Sequence 11, Application US/08609443B
 Patent No. 5840693
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katari
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 APPLICATION NUMBER: US 08/569,063

FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 TISSUE TYPE: human fibrosarcoma
 US-08-609-443B-11

Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 1.2;
 Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;

QY 43 LOEGGQCECKDWFLRAPRRKMTVS-GLPKQCPDHFKNVKKTRHQRHRRKPKHRSR 101
 DB 116 LEEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRDPDPTC 157

QY 102 ACQQLKQCOLRSP 115
 DB 158 RC-----RCRRRSF 166

RESULT 10
 US-08-569-063C-11
 Sequence 11, Application US/08569063C
 Patent No. 5928939
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAJUSOLA, Katari
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/569,063C
 FILING DATE: 06-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP3
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 TISSUE TYPE: human fibrosarcoma
 US-08-569-063C-11

Query Match 10.9%; Score 70; DB 2; Length 188;
 Best Local Similarity 28.4%; Pred. No. 1.2;
 Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;
 QY 43 LOEGQGECECKDWFLAPRRKFTVTS-GLPKQCPDHFKNVKKTRHQRHHRKPKHSR 101
 Db 116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHHQRDPDPTC 157
 QY 102 ACQQLKQCOLRSF 115
 Db 158 RC-----RCRRRSF 166

RESULT 11
 US-08-795-430-57
 Sequence 57, Application US/08795430
 Patent No. 6130071
 GENERAL INFORMATION:
 APPLICANT: Alitalo, Kari
 APPLICANT: Joukov, Vladimir
 TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
 TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/795.430
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FI96/00427
 FILING DATE: 01-AUG-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/671.573
 FILING DATE: 28-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/601.132
 FILING DATE: 14-FEB-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/585.895
 FILING DATE: 12-JAN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/510.133
 FILING DATE: 01-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/340.011
 FILING DATE: 14-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Gass, David A.
 REGISTRATION NUMBER: 38,153
 REFERENCE/DOCKET NUMBER: 28967/33691

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/474-6300
 TELEFAX: 312/474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 188 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-795-430-57

Query Match 10.9%; Score 70; DB 3; Length 188;
 Best Local Similarity 28.4%; Pred. No. 1.2;
 Matches 21; Conservative 12; Mismatches 17; Indels 24; Gaps 5;
 QY 43 LOEGQGECECKDWFLAPRRKFTVTS-GLPKQCPDHFKNVKKTRHQRHHRKPKHSR 101
 Db 116 LEEHSQ-CECR-----PKKDSAVKPSRPLCP-----RCTQHHQRDPDPTC 157
 QY 102 ACQQLKQCOLRSF 115
 Db 158 RC-----RCRRRSF 166

RESULT 12
 US-08-851-896-11
 Sequence 11, Application US/08851896
 Patent No. 6331301
 GENERAL INFORMATION:
 APPLICANT: ERIKSSON, Ulf
 APPLICANT: OLOFSSON, Birgitta
 APPLICANT: ALITALO, Kari
 APPLICANT: PAUSOLA, Katri
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/851,896
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/609,443B
 FILING DATE: 01-MAR-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/397,651
 FILING DATE: 01-MAR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/469,427
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/569,063
 FILING DATE: 06-DEC-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 1064/41979CP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 11:

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30510
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30510

Query Match 10.9%; Score 70; DB 4; Length 626;
Best Local Similarity 29.6%; Pred. No. 5.3;
Matches 29; Conservative 14; Mismatches 33; Indels 22; Gaps 6;

QY 27 GVARG--HRDRGQASR--RWLQGGGQCECKDWFLAPRRKFTVSGLPKQCPDHPKG 82
DB 245 GPAQGLNHVDLEDLERPDRERRDGHQPTQCR---LRPEVQQAAPVSGGRQ----DHHQG 297

QY 83 NVKTRHQ-----RHRKPKKHSRA-----CQOFLKQ 109
DB 298 TEARGHPRAGDVHHRDREHRAQDRHRAQDRHQ 335

Search completed: January 29, 2004, 11:56:45
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 11:48:32 ; Search time 41 Seconds

(without alignments)
460.694 Million cell updates/sec

Title: US-09-786-260-1

Perfect score: 644

Sequence: 1 MKVLISSLLLLPLMLMSV.....SRACQFLKQCQLRSFALPL 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_15Jun03.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644	100.0	119	21	Human secreted pro
2	644	100.0	119	21	Human TGC-440 sec
3	644	100.0	119	21	Human signal pepti
4	644	100.0	119	21	Membrane-bound pro
5	644	100.0	119	22	Human PRO polypept
6	644	100.0	119	22	Amino acid sequenc
7	644	100.0	119	22	Human PRO842. Hom
8	644	100.0	119	22	Human PRO842. UNQ4
9	644	100.0	119	23	Human cytochrome PRO

10	644	100.0	119	23	ABG95863	Human secreted/tra
11	644	100.0	119	24	ABU71181	Human PRO842 prote
12	644	100.0	119	24	ABU71518	Human secreted pol
13	644	100.0	119	24	ABU71964	Novel human secret
14	644	100.0	119	24	ABU72121	Human PRO polypept
15	644	100.0	119	24	ABU65638	Human secreted/tra
16	644	100.0	119	24	ABU65971	Novel human secret
17	644	100.0	119	24	ABU67475	Human secreted/tra
18	644	100.0	119	24	ABU65333	Human PRO polypept
19	644	100.0	119	24	ABU59084	Novel human secret
20	644	100.0	119	24	ABU59231	Human secreted/tra
21	644	100.0	119	24	ABU59380	Novel human secret
22	644	100.0	119	24	ABU60515	Human secreted/tra
23	644	100.0	119	24	ABU58006	Human PRO polypept
24	644	100.0	119	24	ABU58469	Human PRO polypept
25	644	100.0	119	24	ABU58937	Human secreted/tr
26	644	100.0	119	24	ABU56005	Human secreted/tra
27	644	100.0	119	24	ABU57000	Human PRO polypept
28	644	100.0	119	24	ABU13897	Human PRO842 polyp
29	644	100.0	119	24	ABU10579	Human secreted/tra
30	644	100.0	119	24	ABU10852	Human PRO polypept
31	548	85.1	97	21	AAW82454	Mature human TGC-4
32	527	81.8	93	19	AAW83953	Polypeptide encode
33	456	70.8	119	21	AAW82457	Mouse TGC-440 secr
34	386	59.9	97	21	AAW82458	Mature mouse TGC-4
35	386	59.9	119	21	AAW82455	Human 5' EST secre
36	358	55.6	69	20	AAW11732	Mature rat TGC-440
37	342	53.1	97	21	AAW82456	Human secreted pro
38	296	46.0	64	19	AAW83938	Human 5' EST secre
39	225	34.9	48	20	AAW11731	Propionibacterium
40	78.5	12.2	191	22	AAW66308	Part of chick vita
41	73.5	11.4	70	10	AAW91396	Chicken vitamin D
42	73.5	11.4	70	14	AAW43657	Arabidopsis thalia
43	71.5	11.1	108	23	AAW21337	Novel human diagno
44	71	11.0	330	22	ABG25331	Human laminin B2 c
45	71	11.0	1798	19	AAW50896	

ALIGNMENTS

RESULT 1

AAW34728

ID AAB34728 standard; Protein; 119 AA.

XX AAB34728;

AC AAB34728;

XX 26-JAN-2001 (first entry)

XX Human secreted protein encoded by DNA clone vq8 1.

XX Secreted protein; human; autoimmune disorder; multiple sclerosis; ulcer;
XX systemic lupus erythematosus; rheumatoid arthritis; anaemia; stroke;
XX haematopoiesis regulation; tissue regrowth; wound healing; haemophilia;
XX Alzheimer's disease; Parkinson's disease; Shy-drager syndrome; cancer;
XX contraceptive; infection; growth inhibition; hyperproliferative disorder;
XX psoriasis.

XX Hmo sapiens.

XX WO200055375-A1.

XX 21-SEP-2000.

XX 17-MAR-2000; 2000WO-US07285.

XX 17-MAR-1999; 99US-0124808.

XX 17-MAR-1999; 99US-0124916.

XX 17-AUG-1999; 99US-0149639.

XX 01-OCT-1999; 99US-0157247.

XX 29-NOV-1999; 99US-0167824.

XX 15-FEB-2000; 2000US-0182711.

PA (ALPH-) ALPHAGEN INC.
 XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX WPI: 2000-638211/61.
 DR N-PSDB; AAC59829.
 XX Novel proteins and polypeptides useful for the treatment of e.g.
 PT multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis,
 PT cancer, Alzheimer's disease, Parkinson's disease, stroke, anemia and
 PT ulcers
 XX Claim 92; Page 441-442; 493pp; English.
 XX This invention relates to 59 human secreted proteins and the nucleotide
 CC sequences encoding them. Sequences AAC59788-C59846 and AAB34687-B34745
 CC represent the proteins and their encoding nucleotide sequences, and
 CC sequences AAB34746-B34771 represent fragments of the proteins. Probes
 CC for the DNA sequences are represented by sequences AAC59847-C59896. The
 CC proteins exhibit neuroprotective, dermatological, immunosuppressive,
 CC antiinflammatory, antianemic, nootropic, antiparkinsonian,
 CC cerebroprotective, haemostatic, vulnerary, cytostatic, antipsoriatic,
 CC antibacterial, virucide, and fungicide activity. The proteins and
 CC nucleotide sequences are useful as nutritional sources or supplements
 CC in research. The proteins are useful for treating immune deficiency
 CC and disorders, which may be genetic or resulting from infections,
 CC autoimmune disorders such as multiple sclerosis, systemic lupus
 CC erythematosus, rheumatoid arthritis, and for treating myeloid or lymphoid
 CC cell deficiencies such as anaemias by regulating haematopoiesis. The
 CC proteins are also useful in compositions for bone, cartilage, tendon,
 CC ligament and/or nerve tissue growth or regeneration, for wound healing,
 CC tissue repair and replacement and in the treatment of wounds, incisions
 CC and ulcers. Other uses include in the treatment of central and
 CC peripheral nervous system and neuropathies such as Alzheimer's and
 CC Parkinson's diseases and Shy-Drager syndrome, and mechanical and
 CC traumatic disorders, such as spinal cord disorders, head trauma and
 CC stroke. The proteins may also be used as a contraceptive, and for
 CC treating coagulation disorders such as haemophilias. The protein and
 CC nucleotide sequences with cadherin activity are useful for treating
 CC cancer. Other uses for the protein include for inhibiting the growth,
 CC infection or function of, or killing, infectious agents such as bacteria,
 CC virus, fungi and other parasites, for effecting bodily characteristics
 CC such as height, weight, hair colour, effecting biorhythms or cardiac
 CC cycles or rhythms, effecting metabolism, catabolism, anabolism, lipid,
 CC processing, utilization, storage or elimination of dietary fat, lipid,
 CC protein, carbohydrate, vitamins, minerals, cofactors, effecting
 CC behavioural characteristics, providing analgesic effects and for treating
 CC hyperproliferative disorders such as psoriasis.
 XX Sequence 119 AA;
 SQ Query Match 100.0%; Score 644; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQEGGQCECKDWFRLAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQEGGQCECKDWFRLAP 60
 QY 61 RRFMTVSLPKQPCDHFKNVKTTHORHHRKPNKHSRACQFLKQCQLRSFALPL 119
 DB 61 RRFMTVSLPKQPCDHFKNVKTTHORHHRKPNKHSRACQFLKQCQLRSFALPL 119
 RESULT 2
 AAY82453 standard; Protein; 119 AA.
 XX AAY82453;
 XX 30-JUN-2000 (first entry)
 DT Human TGC-440 secretory protein SEQ ID NO:1.
 DE

XX TGC-440; secretory protein; immunological disease; infectious disease;
 KW pulmonary function disorder; hepatic function disorder; nephrotropic;
 KW gastrointestinal function disorder; antiinflammatory; immunomodulatory;
 KW virucide; hepatotropic; antiasthmatic; antibacterial; vaccine;
 KW hepatitis; nephritis; influenza; asthma; pulmonary hypertension;
 KW pneumonia; Helicobacter pylori infection.
 XX Homo sapiens.
 OS WO200014226-A1.
 XX 16-MAR-2000.
 XX 02-SEP-1999; 99WO-JP04765.
 XX 03-SEP-1998; 98JP-0250108.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Itoh Y, Ogi K, Tanaka H, Kitada C;
 XX WPI: 2000-356978/22.
 XX N-PSDB; AAB08343, AAB08344.
 XX Secretory protein TGC440, antibodies to it and compounds promoting or
 PT inhibiting its activity for diagnosis and treatment of diseases of the
 PT immune system, lung, kidney, liver and intestinal system -
 XX Claim 1; Fig 1; 86pp; Japanese.
 XX The present sequence represents a human secretory protein designated
 CC TGC-440. TGC-440 has antiinflammatory, nephrotropic, immunomodulatory,
 CC virucide, hepatotropic, antiasthmatic and antibacterial activities,
 CC and can be used in vaccines. TGC-440 and the polynucleotide sequence
 CC encoding it can be used to treat, prevent and diagnose immunological,
 CC lung, liver, kidney or gastrointestinal disorders and infectious
 CC diseases, such as hepatitis, nephritis, influenza, asthma, pneumonia,
 CC pulmonary hypertension, and Helicobacter pylori infection. An antibody
 CC immunospecific for TGC-440 is also useful in the above treatment and
 CC diagnosis, and also for quantifying the amount of TGC-440 in a liquid
 CC specimen.
 XX Sequence 119 AA;
 SQ Query Match 100.0%; Score 644; DB 21; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQEGGQCECKDWFRLAP 60
 DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRRDQASRWLQEGGQCECKDWFRLAP 60
 QY 61 RRFMTVSLPKQPCDHFKNVKTTHORHHRKPNKHSRACQFLKQCQLRSFALPL 119
 DB 61 RRFMTVSLPKQPCDHFKNVKTTHORHHRKPNKHSRACQFLKQCQLRSFALPL 119
 RESULT 3
 AAY87317 standard; Protein; 119 AA.
 XX AAY87317;
 XX 11-MAY-2000 (first entry)
 DT Human signal peptide containing protein HSP-94 SEQ ID NO:94.
 DE Human; signal peptide-containing protein; HSP-94; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
 KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;

KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX Homo sapiens.
OS WO200000610-A2.
PN 06-JAN-2000.
XX 25-JUN-1999; 99WO-US14484.
XX 26-JUN-1998; 98US-0090762.
PR 31-JUL-1998; 98US-0094983.
PR 01-OCT-1998; 98US-0102686.
PR 11-DEC-1998; 98US-0112129.
XX (INCY-) INCYTE PHARM INC.
PA Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
PI Akertblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX WPI; 2000-160673/14.
DR N-PSDB; AA298202.
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease -
XX Claim 1; Page 220-221; 327pp; English.
XX AA298109 to AA298242 encode AA2987224 to AA2987357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antisthmatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC detecting HSP in standard hybridisation and amplification assays (for
CC nucleic acids can be used for the recombinant production of HSP, for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX Sequence 119 AA;
SQ Query Match 100.0%; Score 644; DB 21; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHGRDQASRRMLQGGQCECKDWFLRAP 60
Db 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHGRDQASRRMLQGGQCECKDWFLRAP 60
QY 61 RKXFWTVSGLPKQPCDDHFGKGVKTKTHORHHRKPKHSRACQQLKQCLRSFALPL 119
Db 61 RKXFWTVSGLPKQPCDDHFGKGVKTKTHORHHRKPKHSRACQQLKQCLRSFALPL 119

RESULT 4
AA2987224
ID AA2987224 standard; protein; 119 AA.
XX AC AA2987224;
XX 05-APR-2000 (first entry)
XX Membrane-bound protein PRO842.
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX Homo sapiens.
OS WO9963088-A2.
PN 09-DEC-1999.
XX 02-JUN-1999; 99WO-US12252.
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088036.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088555.
PR 05-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
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PR 11-JUN-1998; 98US-0088858.
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PR 11-JUN-1998; 98US-0088866.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 15-JUN-1998; 98US-0089440.
PR 15-JUN-1998; 98US-0089512.
PR 15-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.

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PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
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PR 24-JUN-1998; 98US-0090461.
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PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
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PR 25-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091364.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091645.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
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PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 18-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.

PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098553.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX (GETH ) GENENTECH INC.
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
XX N-PSDB; AA265001.
XX
XX Membrane-bound proteins and related nucleotide sequences
XX claim 12; Fig 99; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
XX polynucleotides encoding them. The PRO sequences of the invention were
XX identified based on extracellular domain homology screening. The PRO
XX sequences have homology with proteins including LDL receptors, TIE
XX ligands and various enzymes. The membrane-bound proteins and receptor
XX molecules are useful as pharmaceutical and diagnostic agents. Receptor
XX immunoadhesins, for instance, can be used as therapeutic agents to block
XX receptor-ligand interactions. The membrane-bound proteins can also be
XX employed for screening of potential peptide or small molecule inhibitors
XX of the relevant receptor/ligand interaction. The PRO encoding sequences
XX are useful as hybridization probes, in chromosome and gene mapping and in
XX the generation of antisense RNA and DNA. PRO nucleic acid sequences
XX will also be useful for the preparation of PRO polypeptides, especially
XX by recombinant techniques.
XX
XX Sequence 119 AA;
XX
XX Query Match 100.0%; Score 644; DB 21; Length 119;
XX Best Local Similarity 100.0%; Pred. NO. 1.8e-66;
XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MKVLISLLLLPLMLXSVSSSLNPGVARGHSDRGQASRRMLQEGQCECKDWFRLAP 60
XX Db 1 MKVLISLLLLPLMLXSVSSSLNPGVARGHSDRGQASRRMLQEGQCECKDWFRLAP 60
XX QY 61 RKFMVTSGLPKKQPCDHFKNVKTTHQHHKNTKSHRACQQLKQQLRSFALPL 119
XX Db 61 RKFMVTSGLPKKQPCDHFKNVKTTHQHHKNTKSHRACQQLKQQLRSFALPL 119
XX
XX RESULT 5
XX AAU29093
XX ID AAU29093 standard; Protein; 119 AA.
XX AC AAU29093;
XX
XX XX 18-DEC-2001 (first entry)
XX
XX Human PRO polypeptide sequence #70.
XX
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200168848-A2.
XX
XX
XX
XX

```


QY 61 RRKFTVSGLPKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQLKQQLRSFALPL 119

RESULT 7
AAB87538
ID AAB87538 standard; Protein; 119 AA.

AC AAB87538;
DT 15-MAY-2001 (first entry)
DE Human PRO842.
KW Human; PRO protein; mapping.
OS Homo sapiens.
PN WO200116318-A2.
PD 08-MAR-2001.
PF 24-AUG-2000; 2000WO-US23328.

PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 07-DEC-1999; 99US-0169495.
PR 09-DEC-1999; 99US-0170262.
PR 11-JAN-2000; 2000US-0175461.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 03-MAR-2000; 2000US-0187202.
PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000WO-US14042.
PR 05-JUN-2000; 2000US-0209832.

(GETH) GENENTECH INC.
PA Baton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
N-PSDB; AAF92070.

WPI; 2001-183260/18.
Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
Claim 12; Fig 26; 278pp; English.

The present sequence is a human PRO polypeptide (secreted and transmembrane). The PRO protein, and PRO agonists, PRO antagonists or anti-PRO antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO protein may also be employed as molecular weight markers for protein electrophoresis. The PRO coding sequence has applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping.

Query Match 100.0%; Score 644; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRWLQGGQCECKDWFRLAP 60
DB 1 MKVLISLLLLPLMLMSVSSSLNPGVARGHRDQASRWLQGGQCECKDWFRLAP 60

QY 61 RRKFTVSGLPKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQLKQQLRSFALPL 119
DB 61 RRKFTVSGLPKQPCDHFKNVKKTRHQRHHRKPNKHSRACQQLKQQLRSFALPL 119

RESULT 8
AAB65191
ID AAB65191 standard; Protein; 119 AA.

AC AAB65191;
DT 02-APR-2001 (first entry)
DE Human PRO842 (UNQ473) protein sequence SEQ ID NO:165.
KW Human; secreted and transmembrane protein; PRO; cytosstatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing; diagnostic assay.
OS Homo sapiens.
PN WO200073454-A1.
PD 07-DEC-2000.

PF 30-MAR-2000; 2000WO-US08439.
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.
PA Askenazi AJ, Baker KP, Borstein D, Deasnovers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, KJavlin IJ, Napier MA, Pan J, Paoni NP;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
WPI; 2001-032160/04.
DR N-PSDB; AAF44147.

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
Claim 12; Fig 99; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cyrostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAF55154 to AAF55300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

XX SQ Sequence 119 AA;
Query Match 100.0%; Score 644; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Db 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Qy 61 RRKFMTVSGLPKKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119
Db 61 RRKFMTVSGLPKKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 9
ABP54931
ID ABP54931 standard; Protein; 119 AA.
XX AC ABP54931;
XX DT 08-JAN-2003 (first entry)
XX DE Human cytokine PRO842 (CK27).
XX KW PRO842; CK27; chemokine; human; antiinflammatory; dermatological;
KW hepatocytic; antiasthmatic; antidiabetic; immunosuppressive;
KW antirheumatic; antiarthritic; nephrotropic.

XX OS Homo sapiens.
XX FH Location/Qualifiers
FT Key 1..22
FT Peptide /label= Signal_peptide
FT Protein 23..119
FT /label= Mature_protein
FT Modified-site 27..32
FT /note= "potential N-myristoylation site"
FT Modified-site 39..41
FT /note= "potential protein kinase C phosphorylation site"
FT Modified-site 46..51
FT /note= "potential N-myristoylation site"
XX WO20020706-A2.
XX PD 12-SEP-2002.
XX PF 07-DEC-2001; 2001WO-US48060.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 28-AUG-2001; 2001US-0941992.
XX PA (GETH) GENENTECH INC.
XX PI French D, Grimaldi JC, Hillian KJ, Pisabarro MT, Schmidt KN;
PI Smith V, Tumas D, Vandlen RL, Watanabe CK, Williams EM, Wood WI;
XX WPI: 2002-750461/81.
XX DR N-PSDB; ABV73914.

PT New PRO842 polypeptides having structural homology to interleukin-8,
PT useful for treating or diagnosing a mammal with an inflammatory disease
PT or immune related disease, e.g. rheumatoid arthritis, osteoarthritis or
PT allergic disease

XX Claim 1; Fig 2; 118pp; English.

XX The present sequence is the protein sequence of PRO842 (CK27),
XX a novel human chemokine (mol.wt. 13.8 kDa, pI 11.16) having
XX structural homology to interleukin-8. Microarray analysis has
XX shown PRO842 to be over-expressed in colon tumour, lung tumour and
XX breast tumour cells compared with non-cancerous human tissue,
XX making it a useful diagnostic marker for cancerous tumours and a
XX therapeutic target. PRO842 also plays a role in the inflammatory
XX response, having chemoattractant properties toward monocytes and
XX dendritic cells. The invention provides PRO842 polypeptides,
XX polynucleotides, host cells, vectors and antibodies, as well as
XX methods of treating an immune related disorder by using a PRO842
XX polypeptide, or an agonist, antagonist or antibody. The immune
XX related disorder may be systemic lupus erythematosus, rheumatoid
XX arthritis, osteoarthritis, juvenile chronic arthritis,
XX spondyloarthritis, systemic sclerosis, idiopathic inflammatory
XX myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
XX autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
XX thyroiditis, diabetes mellitus, immune-mediated renal disease,
XX demyelinating disease of the central or peripheral nervous system,
XX idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX chronic inflammatory demyelinating polyneuropathy, hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous
XX skin disease, erythema multiforme, contact dermatitis, psoriasis,
XX an allergic disease, asthma, allergic rhinitis, atopic dermatitis,
XX food hypersensitivity, urticaria, an immunologic disease of the
XX ovaries, an immunologic disease of the lung, eosinophilic
XX pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX pneumonitis, a transplantation associated disease, graft rejection
XX or graft-versus-host-disease (all claimed).

XX SQ Sequence 119 AA;

Query Match 100.0%; Score 644; DB 23; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Db 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
Qy 61 RRKFMTVSGLPKKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119
Db 61 RRKFMTVSGLPKKQCPDHFKNVKKTRHQRHRRKPNKHSRACQFLKQCQLRSFALPL 119

RESULT 10
ABG95863
ID ABG95863 standard; Protein; 119 AA.

XX AC ABG95863;
XX DT 10-DEC-2002 (first entry)
XX DE Human secreted/transmembrane protein PRO842.
XX KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX OS Homo sapiens.
XX PN US2002119130-A1.

PD 29-AUG-2002.
 XX 06-DEC-2001; 2001US-0006867.
 XX 29-OCT-1997; 97US-063435P.
 PR 29-OCT-1997; 97US-064215P.
 PR 22-APR-1998; 98US-082797P.
 PR 29-APR-1998; 98US-083495P.
 PR 15-MAY-1998; 98US-085519P.
 PR 10-JUN-1998; 98US-088811P.
 PR 10-JUN-1998; 98US-088824P.
 PR 10-JUN-1998; 98US-088825P.
 PR 11-JUN-1998; 98US-088863P.
 PR 12-JUN-1998; 98US-089105P.
 PR 16-JUN-1998; 98US-089514P.
 PR 16-SEP-1998; 98WO-US19330.
 PR 08-MAR-1999; 98WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21194.
 PR 22-DEC-1999; 99WO-US30720.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32378.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 XX
 XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX

DR WPI; 2002-731348/79.
 DR N-PSDB; ABS74390.

XX New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis

XX Claim 20; Fig 26; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing
 CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
 CC an extracellular domain of the proteins with their associated signal
 CC peptide or lacking its associated signal peptide. Also included are
 CC the nucleic acids encoding the proteins, vectors, host cells,
 CC fusion proteins and antibodies which specifically bind to the proteins.
 CC The proteins are useful for detecting a polypeptide designated as A, B, C
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,
 CC by contacting the sample with a polypeptide designated as E, F, G, H or
 CC I (or vice versa) and determining the formation of a A/E, B/F, C/H
 CC or D/I polypeptide conjugate in the sample, where the formation of the
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
 CC polypeptide, C is a PRO10036 polypeptide, D is a PRO19760 polypeptide,
 CC E is a PRO3801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
 CC polypeptide, H is a PRO20233 polypeptide and I is a PRO1890
 CC polypeptide. The sample comprises a cell suspected of expressing the A,
 CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
 CC a detectable label or is attached to a solid support. The proteins are
 CC useful for linking a bioactive molecule to a cell expressing a

CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
 CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
 CC against them are useful for modulating a biological activity of a cell
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
 CC I. The cell is killed. The proteins are useful for identifying
 CC agonists or antagonists, for the preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the proteins, as
 CC molecular weight markers for protein electrophoresis purposes, and as
 CC therapeutic agents for treating sports-related joint problems, and as
 CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.
 CC Nucleic acids encoding the proteins are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of anti-sense RNA and
 CC DNA, for the preparation of the proteins, to generate transgenic or
 CC knockout animals which are useful in the development and screening of
 CC therapeutic useful reagents, for chromosome identification, and in gene
 CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic
 CC assay and for affinity purification of the protein from recombinant
 CC cell culture natural sources. The present sequence represents a novel
 CC secreted or transmembrane protein of the invention.

XX Sequence 119 AA;

Query Match 100.0%; Score 644; DB 23; Length 119;
 Best Local Similarity 100.0%; Pred.No.1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISLLLLFLMLSMVSSSLNFGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
 Db 1 MKVLISLLLLFLMLSMVSSSLNFGVARGHRDRGQASRRWLQGGQCECKDWFLRAP 60
 QY 61 RRKFWTVSGLPKQCPCDHFKNVKKTRKHRRKPKNSRACQFLKQCOLRSPALPL 119
 Db 61 RRKFWTVSGLPKQCPCDHFKNVKKTRKHRRKPKNSRACQFLKQCOLRSPALPL 119

RESULT 11

ABU71181
 ID ABU71181 standard; Protein; 119 AA.
 XX
 AC ABU71181;
 XX
 DT 10-JUN-2003 (first entry)
 XX
 DE Human PRO842 protein.
 XX
 KW Human; PRO; secreted; transmembrane; cytostatic; TNF-alpha; blood;
 KW tumour necrosis factor alpha release; chondrocyte cell; proliferation;
 KW differentiation; tumour; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2003036143-A1.
 XX 20-FEB-2003.
 PD
 PF 02-JUL-2002; 2002US-0187600.
 XX
 PR 16-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 08-MAR-1999; 99WO-US05028.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 01-DEC-1999; 99WO-US28301.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.

PR	24-FEB-2000;	2000WO-US05004.	PR	15-MAY-1998;	98US-085700P.
PR	01-MAR-2000;	2000WO-US05601.	PR	18-MAY-1998;	98US-086032P.
PR	02-MAR-2000;	2000WO-US05841.	PR	22-MAY-1998;	98US-086332P.
PR	15-MAR-2000;	2000WO-US06884.	PR	22-MAY-1998;	98US-087098P.
PR	30-MAR-2000;	2000WO-US08439.	PR	28-MAY-1998;	98US-087208P.
PR	17-MAY-2000;	2000WO-US11705.	PR	28-MAY-1998;	98US-087609P.
PR	22-MAY-2000;	2000WO-US14042.	PR	02-JUN-1998;	98US-087759P.
PR	30-MAY-2000;	2000WO-US14941.	PR	03-JUN-1998;	98US-087827P.
PR	02-JUN-2000;	2000WO-US15264.	PR	04-JUN-1998;	98US-088025P.
PR	28-JUL-2000;	2000WO-US20710.	PR	04-JUN-1998;	98US-088028P.
PR	24-AUG-2000;	2000WO-US23328.	PR	04-JUN-1998;	98US-088029P.
PR	08-NOV-2000;	2000WO-US30952.	PR	04-JUN-1998;	98US-088033P.
PR	01-DEC-2000;	2000WO-US32678.	PR	04-JUN-1998;	98US-088326P.
PR	20-DEC-2000;	2000WO-US34956.	PR	05-JUN-1998;	98US-088167P.
PR	28-FEB-2001;	2001WO-US06520.	PR	05-JUN-1998;	98US-088202P.
PR	01-JUN-2001;	2001WO-US17800.	PR	05-JUN-1998;	98US-088212P.
PR	20-JUN-2001;	2001WO-US19692.	PR	05-JUN-1998;	98US-088212P.
PR	29-JUN-2001;	2001WO-US21066.	PR	09-JUN-1998;	98US-088655P.
PR	09-JUL-2001;	2001WO-US22106.	PR	10-JUN-1998;	98US-088732P.
PR	29-AUG-2001;	2001WO-US21735.	PR	10-JUN-1998;	98US-088739P.
PR	18-SEP-1997;	97US-059263P.	PR	10-JUN-1998;	98US-088740P.
PR	18-SEP-1997;	97US-059266P.	PR	10-JUN-1998;	98US-088811P.
PR	17-OCT-1997;	97US-062250P.	PR	10-JUN-1998;	98US-088824P.
PR	21-OCT-1997;	97US-063486P.	PR	10-JUN-1998;	98US-088825P.
PR	24-OCT-1997;	97US-063120P.	PR	10-JUN-1998;	98US-088826P.
PR	24-OCT-1997;	97US-063121P.	PR	11-JUN-1998;	98US-088861P.
PR	28-OCT-1997;	97US-063540P.	PR	11-JUN-1998;	98US-088863P.
PR	28-OCT-1997;	97US-063541P.	PR	11-JUN-1998;	98US-088876P.
PR	28-OCT-1997;	97US-063544P.	PR	11-JUN-1998;	98US-089090P.
PR	29-OCT-1997;	97US-063734P.	PR	12-JUN-1998;	98US-089105P.
PR	31-OCT-1997;	97US-063870P.	PR	12-JUN-1998;	98US-089122P.
PR	31-OCT-1997;	97US-064103P.	PR	16-JUN-1998;	98US-089514P.
PR	13-NOV-1997;	97US-065311P.	PR	17-JUN-1998;	98US-089538P.
PR	21-NOV-1997;	97US-066120P.	PR	17-JUN-1998;	98US-089598P.
PR	24-NOV-1997;	97US-066466P.	PR	17-JUN-1998;	98US-089653P.
PR	24-NOV-1997;	97US-065772P.	PR	18-JUN-1998;	98US-089908P.
PR	11-DEC-1997;	97US-069335P.	PR	19-JUN-1998;	98US-089952P.
PR	12-DEC-1997;	97US-069425P.	PR	22-JUN-1998;	98US-090246P.
PR	17-DEC-1997;	97US-069870P.	PR	22-JUN-1998;	98US-090252P.
PR	18-DEC-1997;	97US-068017P.	PR	22-JUN-1998;	98US-090254P.
PR	10-MAR-1998;	98US-077450P.	PR	24-JUN-1998;	98US-090429P.
PR	11-MAR-1998;	98US-077532P.	PR	24-JUN-1998;	98US-090435P.
PR	11-MAR-1998;	98US-077649P.	PR	24-JUN-1998;	98US-090444P.
PR	20-MAR-1998;	98US-078886P.	PR	24-JUN-1998;	98US-090461P.
PR	27-MAR-1998;	98US-078939P.	PR	24-JUN-1998;	98US-090533P.
PR	27-MAR-1998;	98US-079664P.	PR	24-JUN-1998;	98US-090540P.
PR	27-MAR-1998;	98US-079786P.	PR	25-JUN-1998;	98US-090676P.
PR	31-MAR-1998;	98US-080107P.	PR	25-JUN-1998;	98US-090678P.
PR	31-MAR-1998;	98US-080194P.	PR	25-JUN-1998;	98US-090688P.
PR	01-APR-1998;	98US-080327P.	PR	25-JUN-1998;	98US-090690P.
PR	01-APR-1998;	98US-080333P.	PR	25-JUN-1998;	98US-090694P.
PR	08-APR-1998;	98US-081070P.	PR	25-JUN-1998;	98US-090695P.
PR	08-APR-1998;	98US-081099P.	PR	25-JUN-1998;	98US-090698P.
PR	09-APR-1998;	98US-081195P.	PR	26-JUN-1998;</	

PR 18-AUG-1998; 98US-096949P.
PR 18-AUG-1998; 98US-096959P.
PR 18-AUG-1998; 98US-097022P.
PR 26-AUG-1998; 98US-097952P.
PR 26-AUG-1998; 98US-097953P.
PR 26-AUG-1998; 98US-097954P.
PR 26-AUG-1998; 98US-097955P.
PR 26-AUG-1998; 98US-097971P.
PR 26-AUG-1998; 98US-097974P.
PR 26-AUG-1998; 98US-098014P.
PR 01-SEP-1998; 98US-098716P.
PR 01-SEP-1998; 98US-098723P.
PR 02-SEP-1998; 98US-098803P.
PR 02-SEP-1998; 98US-098821P.
PR 02-SEP-1998; 98US-098843P.
PR 09-SEP-1998; 98US-099602P.
PR 10-SEP-1998; 98US-099741P.
PR 10-SEP-1998; 98US-099754P.
PR 10-SEP-1998; 98US-099763P.
PR 10-SEP-1998; 98US-099812P.

Query Match 100.0%; Score 644; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDGOASRWLQEGQCECKDWFRLAP 60
DB 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDGOASRWLQEGQCECKDWFRLAP 60
QY 61 RKFTMTVSGLPKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQQLKQQLRSFALPL 119
DB 61 RKFTMTVSGLPKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQQLKQQLRSFALPL 119

RESULT 12
ABU71518
ID ABU71518 standard; Protein; 119 AA.
XX
AC ABU71518;
DT 10-JUN-2003 (first entry)
DE Human secreted polypeptide PR0842.
XX
KW Human; gene therapy; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003013855-A1.
XX
PD 16-JAN-2003.
XX
PF 03-MAY-2002; 2002US-0063616.
XX
PR 30-DEC-1998; 98XR-0062142.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 21-MAR-2000; 2000WO-US07532.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US14264.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 14-MAY-1999; 98US-0311832.
PR 25-AUG-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.

PR 25-AUG-1999; 99US-0380142.
PR 15-SEP-1999; 99US-0397342.
PR 18-OCT-1999; 99US-0403297.
PR 12-NOV-1999; 99US-0423844.
PR 22-AUG-2000; 2000US-064848.
PR 18-SEP-2000; 2000US-0664810.
PR 18-SEP-2000; 2000US-0665350.
PR 08-NOV-2000; 2000US-0709238.
PR 20-DEC-2000; 2000US-0747259.
PR 22-MAR-2001; 2001US-0816744.
PR 10-MAY-2001; 2001US-0854208.
PR 30-MAY-2001; 2001US-0854280.
PR 05-JUN-2001; 2001US-0870574.
PR 29-JUN-2001; 2001US-0874503.
PR 18-JUL-2001; 2001US-0869599.
PR 06-DEC-2001; 2001US-0908827.
XX
PA (GETH) GENENTECH INC.
XX
PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX
DR WPI; 2003-330485/31.
DR N-PSDB; ACA58822.
XX
PT New isolated antibody specifically binding a PRO polypeptide, useful
PT for the preparation of a medicament for treating disorders with the
PT aberrant expression or activity of the PRO polypeptide, such as tumor
PT conditions and cancer -
XX
PS Disclosure; Page 93; 406pp; English.
XX
CC The invention relates to an antibody that binds to a polypeptide with a
CC fully defined sequence given in the specification. The methods and
CC compositions (containing antibodies that specifically bind a PRO
CC polypeptide) of the present invention are useful for the preparation of a
CC medicament for the treatment of disorders associated with the aberrant
CC expression or activity of the PRO polypeptide, such as tumour conditions
CC and cancer. They can also be used to generate transgenic or knockout
CC animals useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides and encoding nucleic acids can be used as
CC molecular weight markers for protein electrophoresis, chromosome
CC identification and tissue typing. The PRO polypeptides are useful to
CC induce angiogenesis e.g wound healing; in the treatment of sports-related
CC joint problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis; diabetes; hyperinsulinaemia and hypoinsulinaemia. The
CC antibodies may be used in various diagnostic, competitive binding and/or
CC immunoprecipitation assays. The present sequence represents the amino
CC acid sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 644; DB 24; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.8e-66;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDGOASRWLQEGQCECKDWFRLAP 60
DB 1 MKVLISLLILLPLMLSMVSSSLNPGVARGHRRDGOASRWLQEGQCECKDWFRLAP 60
QY 61 RKFTMTVSGLPKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQQLKQQLRSFALPL 119
DB 61 RKFTMTVSGLPKQPCDHFHFGKGNVKKTRHQRHRRKPNKHSRACQQLKQQLRSFALPL 119

RESULT 13
ABU71964
ID ABU71964 standard; Protein; 119 AA.
XX
AC ABU71964;
XX
DT 11-JUN-2003 (first entry)

XX DE Novel human secreted and transmembrane protein PRO842.
 XX XX Human; secreted and transmembrane polypeptide;
 XX KW chromosome mapping; gene mapping; transgenic animal; knockout animal;
 XX KW therapeutic agent screening; chromosome identification; tissue typing;
 XX KW gene therapy.
 XX OS Homo sapiens.
 XX PN US2003018183-A1.
 XX PD 23-JAN-2003.
 XX PF 01-MAY-2002; 2002US-0063512.
 XX PR 06-DEC-2001; 2001US-0006867.
 XX PA (GETH) GENENTECH INC.
 XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX DR WPI; 2003-330984/31.
 XX DR N-PSDB; ACA60375.
 XX PT New secreted and transmembrane PRO polypeptides and nucleic acid
 PT molecules encoding the polypeptides, useful in gene therapy or
 PT preparing a medicament for treating a condition that is responsive to
 PT the PRO polypeptide or antibody -
 XX PS Disclosure; Fig 26; 409pp; English.
 XX CC The invention describes novel isolated PRO polypeptides. The PRO
 CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
 CC for treating a condition that is responsive to the PRO polypeptide or
 CC antibody. The PRO nucleotide sequences may be used as hybridisation
 CC probes in chromosome and gene mapping, or in generating antisense RNA
 CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
 CC in assays to identify other proteins or molecules involved in binding
 CC reaction, to generate transgenic animals or knockout animals, which in
 CC turn are useful in the development and screening of therapeutically
 CC useful reagents, for chromosome identification, and tissue typing. The
 CC PRO polypeptides and nucleic acid molecules are also useful in gene
 CC therapy, and as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. This is the amino acid sequence of a novel
 CC human secreted and transmembrane PRO polypeptide.
 XX XX
 XX SQ Sequence 119 AA;
 Query Match 100.0%; Score 644; DB 24; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 Db 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 QY 61 RRKFMTVSGLPKQPCDHFPGNVKTKTHQRRHKPNKHSRACQQLKQCLRSFALPL 119
 Db 61 RRKFMTVSGLPKQPCDHFPGNVKTKTHQRRHKPNKHSRACQQLKQCLRSFALPL 119
 RESULT 14
 ABU72121
 ID ABU72121 standard; Protein; 119 AA.
 XX AC
 XX AC ABU72121;
 XX DT 13-JUN-2003 (first entry)
 XX OS Homo sapiens.

DE Human PRO polypeptide #13.
 XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW anti-PRO antibody; diagnostic assay; gene expression.
 XX OS Homo sapiens.
 XX PN US2003023042-A1.
 XX PD 30-JAN-2003.
 XX PF 01-MAY-2002; 2002US-0063502.
 XX PR 06-DEC-2001; 2001US-0006867.
 XX PA (GETH) GENENTECH INC.
 XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX DR WPI; 2003-331484/31.
 XX DR N-PSDB; ACA63385.
 XX PT Novel monoclonal antibody that binds to secreted and transmembrane
 PT polypeptide, useful for detecting and purifying the polypeptide and
 PT also for treating conditions responsive to the antibody -
 XX PS Disclosure; Fig 26; 408pp; English.
 XX CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides and polynucleotides are useful for preparing a
 CC medicament useful in the treatment of a condition responsive to
 CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
 CC assays for PRO, by detecting its expression in specific cells,
 CC tissues or serum, and for affinity purification of PRO from
 CC recombinant cell culture or natural sources. ABU72109-ABU72192
 CC represent the human PRO polypeptides of the invention.
 XX XX
 XX SQ Sequence 119 AA;
 Query Match 100.0%; Score 644; DB 24; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 Db 1 MKVLISSLLLLPLMLMSVSSSLNPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAP 60
 QY 61 RRKFMTVSGLPKQPCDHFPGNVKTKTHQRRHKPNKHSRACQQLKQCLRSFALPL 119
 Db 61 RRKFMTVSGLPKQPCDHFPGNVKTKTHQRRHKPNKHSRACQQLKQCLRSFALPL 119
 RESULT 15
 ABU65638
 ID ABU65638 standard; Protein; 119 AA.
 XX AC
 XX AC ABU65638;
 XX DT 19-MAY-2003 (first entry)
 XX DE Human secreted/transmembrane protein, SEQ ID 140.
 XX KW Human; PRO; secreted protein; transmembrane protein;
 KW cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW cervical tumour; liver tumour; TNF-alpha release; arthritis;
 KW tumour necrosis factor alpha; chondrocyte cell; bone disorder;
 KW cartilage disorder; sports injury.
 XX OS Homo sapiens.

XX US2003036156-A1.
PN 20-FEB-2003.
XX 02-JUL-2002; 2002US-0188767.
XX 16-SEP-1998; 98WO-US9330.
PR 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28551.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 29-AUG-2001; 2001WO-US27099.
PR 18-SEP-1997; 97US-059263P.
PR 18-SEP-1997; 97US-059266P.
PR 17-OCT-1997; 97US-062250P.
PR 21-OCT-1997; 97US-063486P.
PR 24-OCT-1997; 97US-063120P.
PR 24-OCT-1997; 97US-063121P.
PR 28-OCT-1997; 97US-063540P.
PR 28-OCT-1997; 97US-063541P.
PR 28-OCT-1997; 97US-063544P.
PR 28-OCT-1997; 97US-063564P.
PR 29-OCT-1997; 97US-063734P.
PR 31-OCT-1997; 97US-063670P.
PR 31-OCT-1997; 97US-064103P.
PR 13-NOV-1997; 97US-065311P.
PR 21-NOV-1997; 97US-066120P.
PR 24-NOV-1997; 97US-066466P.
PR 24-NOV-1997; 97US-066772P.
PR 11-DEC-1997; 97US-069335P.
PR 12-DEC-1997; 97US-069425P.
PR 17-DEC-1997; 97US-069870P.
PR 18-DEC-1997; 97US-068017P.
PR 10-MAR-1998; 98US-077450P.
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PR 01-APR-1998; 98US-080327P.
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PR 08-APR-1998; 98US-081049P.
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PR 03-JUN-1998; 98US-087827P.
PR 04-JUN-1998; 98US-088025P.
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PR 10-JUN-1998; 98US-088825P.
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PR 12-JUN-1998; 98US-089090P.
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PR 25-JUN-1998; 98US-090685P.
PR 25-JUN-1998; 98US-090690P.

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PR	25-JUN-1998;	98US-090696P.
PR	26-JUN-1998;	98US-090862P.
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PR	01-JUL-1998;	98US-091359P.
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PR	17-AUG-1998;	98US-096757P.
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PR	26-AUG-1998;	98US-097971P.
PR	26-AUG-1998;	98US-097974P.
PR	26-AUG-1998;	98US-098014P.
PR	01-SEP-1998;	98US-098716P.
PR	01-SEP-1998;	98US-098723P.
PR	02-SEP-1998;	98US-098803P.
PR	02-SEP-1998;	98US-098821P.
PR	02-SEP-1998;	98US-098843P.
PR	09-SEP-1998;	98US-099602P.
PR	10-SEP-1998;	98US-099741P.
Query Match 100.0%; Score 644; DB 24; Length 119;		
Best Local Similarity 100.0%; Pred. No. 1.8e-66;		
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	MKVLISLLILLPLMLMSVSSSLNPGVARGHRRDRGQASRRWLQGGQCECKDWFLRAP 60
Db	1	MKVLISLLILLPLMLMSVSSSLNPGVARGHRRDRGQASRRWLQGGQCECKDWFLRAP 60
Qy	61	RRKFTVSGLPKQCPDHFKNVKKTRHORHRRKPKHRSRACQQLKQQLRSFALPL 119
Db	61	RRKFTVSGLPKQCPDHFKNVKKTRHORHRRKPKHRSRACQQLKQQLRSFALPL 119

Search completed: January 29, 2004, 11:54:25
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 11:52:13 ; Search time 35 Seconds
(without alignments)
877,379 Million cell updates/sec

Title: US-09-786-260-1
Perfect score: 644
Sequence: 1 MKVLISLLILLPLMLMSV.....SPACQFLKQCLRSFALPL 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mnc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	322	50.0	128	11 Q8R3U6	Q8R3U6 mus musculus
2	77.5	12.0	337	5 O62022	O62022 caenorhabdi
3	77.5	12.0	449	5 Q810M4	Q810M4 caenorhabdi
4	76.5	11.9	411	13 Q9W745	Q9W745 xenopus lae
5	72.5	11.3	752	4 Q8NAP3	Q8NAP3 homo sapien
6	71.5	11.1	108	10 Q82328	Q82328 arabidopsis
7	71	11.0	188	4 Q8TSV2	Q8TSV2 homo sapien
8	71	11.0	543	5 Q8MQJ1	Q8MQJ1 drosophila
9	71	11.0	3190	5 O01368	O01368 drosophila
10	71	11.0	3276	5 Q9W321	Q9W321 drosophila
11	70.5	10.9	160	10 Q9SQH1	Q9SQH1 arachis hyp
12	70.5	10.9	1290	3 Q96UA3	Q96UA3 neurospora
13	70	10.9	117	4 Q9BRN8	Q9BRN8 homo sapien
14	70	10.9	743	5 Q97120	Q97120 schistosoma
15	70	10.9	746	5 Q8INJ0	Q8INJ0 drosophila
16	70	10.9	1095	5 Q21852	Q21852 caenorhabdi

17	70	10.9	1564	5 Q9TVQ2	Q9TVQ2 caenorhabdi
18	69.5	10.8	221	12 Q85299	Q85299 ori virus.
19	69.5	10.8	468	4 Q9UC32	Q9UC32 homo sapien
20	69.5	10.8	625	4 Q8IV29	Q8IV29 homo sapien
21	69.5	10.8	653	12 Q8JTG6	Q8JTG6 human papil
22	69	10.7	111	10 Q9FWY9	Q9FWY9 oryza sativ
23	69	10.7	200	16 Q9HVU8	Q9HVU8 pseudomonas
24	69	10.7	271	4 Q9HBS0	Q9HBS0 homo sapien
25	69	10.7	378	3 O74213	O74213 aspergillus
26	69	10.7	400	10 Q8LEL2	Q8LEL2 arabidopsis
27	69	10.7	413	10 Q9C8W2	Q9C8W2 arabidopsis
28	69	10.7	454	13 Q90ZB8	Q90ZB8 oncorhynch
29	69	10.7	527	10 Q9SKW4	Q9SKW4 arabidopsis
30	69	10.7	1077	4 Q8N279	Q8N279 homo sapien
31	69	10.7	1081	5 Q8BE73	Q8BE73 macaca fasc
32	68.5	10.6	381	5 Q86641	Q86641 strongyloce
33	68.5	10.6	405	13 Q9PS79	Q9PS79 xenopus . xc
34	68.5	10.6	422	11 Q922X0	Q922X0 mus musculu
35	68.5	10.6	427	6 Q95MH5	Q95MH5 saguinus ce
36	68.5	10.6	1006	16 P73012	P73012 synchocyst
37	68	10.6	189	14 Q99IU7	Q99IU7 uncultured
38	68	10.6	283	10 Q43508	Q43508 lycopersico
39	68	10.6	291	13 Q9IAK3	Q9IAK3 xenopus lae
40	68	10.6	539	10 Q9XHV3	Q9XHV3 oryza sativ
41	67.5	10.5	453	13 Q9PTN2	Q9PTN2 brachydanio
42	67.5	10.5	1069	5 Q8BPS2	Q8BPS2 bombyx mori
43	67	10.4	376	10 Q9LXW3	Q9LXW3 arabidopsis
44	67	10.4	454	13 Q8QGE2	Q8QGE2 salmo salar
45	67	10.4	743	12 Q83111	Q83111 mouse adeno

ALIGNMENTS

RESULT 1

Q8R3U6 PRELIMINARY; PRT; 128 AA.

AC Q8R3U6; DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Similar to hypothetical gene LOC125944.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBAJ databases.
DR EMBL; BC024561; AAH24561.1; -- CCE67DA04D23D7DF CRC64;
SQ SEQUENCE 128 AA; 14043 MW; CCE67DA04D23D7DF CRC64;

Query Match 50.0%; Score 322; DB 11; Length 128;
Best Local Similarity 70.9%; Pred. No. 7.1e-30;
Matches 61; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MKVLISLLILLPLMLMSVSSLNPGVARGHREGQASREWLQEGGCECKDWEFLRAP 60
Db	1	MKLLASFPFLLLPVLMMSVFPSPNGVARGHGOHLAPRWLLEGGCECKDWEFLQAP 60
Qy	61	RRKFTMTVSGLPKQPCDHFKNVKK 86
Db	61	KRKATAVLGPRKQPCDHFKNVKK 86

RESULT 2

O62022 PRELIMINARY; PRT; 337 AA.

ID O62022; O18293;
AC O62022; DT 01-AUG-1998 (TREMELrel. 07, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)


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[1]
RN RP SEQUENCE FROM N.A.
RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Tissue=Brain;
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saiko K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Negai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AK092355; BAC03868.1; -
DR InterPro: IPR007087; Znf_C2H2.
DR Pfam: PF000096; zf-C2H2; 1.
DR SMART: SM00355; ZNF_C2H2; 1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 5.
KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
FT NON TER 752
SQ SEQUENCE 752 AA; 84142 MW; 3CB567B2B8155A8 CRC64;

Query Match 11.3%; Score 72.5; DB 4; Length 752;
Best Local Similarity 28.0%; Pred. No. 7.6;
Matches 26; Conservative 16; Mismatches 36; Indels 15; Gaps 3;

QY 5 ISSLLILLPLMLSMVSSSINPVGARHGDRGQASRRWLQGGQCECKDWFLAPRRKF 64
Db 55 ISKLKLLKYLIIISTVPQSLSS-----RDKQSLISQLQE-----KSEYRSWTKLL 100

QY 65 MTGVSGLKQKQPCDHPKGN-VKTRHQRHRRKP 96
Db 101 IATSQIPRVPMYSVLKREWLKKKKRHEEP 133

RESULT 6
O82328 PRELIMINARY; PRT; 108 AA.
AC O82328;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE GAST1/GASA-like protein.
GN At2G14900.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.s.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=2083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.D., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Bisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequencing and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AC005396; AAC61287.1; -
DR InterPro: IPR003854; GASA.
DR Pfam: PF02704; GASA; 1.
SQ SEQUENCE 108 AA; 11381 MW; 93206EAE3BB95DF5 CRC64;
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Query Match 11.1%; Score 71.5; DB 10; Length 108;
Best Local Similarity 25.9%; Pred. No. 1.3;
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY 1 MKVLSSILL-LPLMLSMVSSSINPVGAR-----HSDRGASRRWLQGGQCE-- 51
Db 1 MKIIIVIIIVLASLLISSLASATISDAFGGAVAPAQSKDGPALBKWC---GQCEGR 57

QY 52 CXDWFLAPRRKFTVSGLPKKQKQPCDHPKGNVKKTRHQRHRRKPKHRSRAC 103
Db 58 CXE---AGMKDRCLKYCIGCKDQC-----VPSGTV-----GNKHECAC 94

RESULT 7
O8TEV2 PRELIMINARY; PRT; 188 AA.
ID O8TEV2;
AC O8TEV2;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Vascular endothelial growth factor B isoform VEGF-B167.
GN VEGFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chilov D., Alitalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
endothelial growth factor B (VEGF-B) and characterization of a second
splice isoform.";
RT splice isoform.
RL J. Biol. Chem. 271:19310-19317 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98032228; PubMed=9365524;
RA Joukov V., Kaipainen A., Jeltsch M., Pajusola K., Olofsson B.,
RA Kumar V., Eriksson U., Alitalo K.;
RT "Vascular endothelial growth factors VEGF-B and VEGF-C.";
RL J. Cell. Physiol. 173:211-215 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Jeltsch M., Pajusola K., Chilov D., Alitalo K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF468110; AAL79000.1; -
DR InterPro: IPR002400; GF_cycknot.
DR InterPro: IPR000072; PD_growth_factor.
DR Pfam: PF00341; PDGF; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD001629; PD_growth_factor; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS00249; PDGF_1; 1.
DR PROSITE: PS0278; PDGF_2; 1.
SQ SEQUENCE 188 AA; 21314 MW; F04654D5A3626095 CRC64;

Query Match 11.0%; Score 71; DB 4; Length 188;
Best Local Similarity 29.7%; Pred. No. 2.7;
Matches 22; Conservative 13; Mismatches 15; Indels 24; Gaps 6;

QY 43 LQEGQCECECKDWFLAPRRKFTVSGLPKKQKQPCDHPKGNVKKTRHQRHRRKPKHRSR 101
Db 116 LEHSQ-CECR-----PKKDSAVKPDSPRLCP-----RCTQHQRPD--PR 155

QY 102 ACQQLKQCLRSR 115
Db 156 TCR---RRCRRRSF 166

RESULT 8
O8MQJ1 PRELIMINARY; PRT; 543 AA.
ID O8MQJ1
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AC O8MQJ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RE08410p.
GN SVP OR CG11502 OR CG18158.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brockstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AV129452; AAM76194.1; -.
DR FlyBase; FBgn003651; svp.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhmr_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 543 AA; 58047 MW; DD04FD10042C2D3C CRC64;

Query Match 11.0%; Score 71; DB 5; Length 543;
Best Local Similarity 26.7%; Pred. No. 8.1;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSNPG-----VAHGHRDRGQASRRWLQEGGQCECKDWFLRAPRRKFTMTVSG 69
Db 183 SSSNSGQIDSKQNIQVVGDKSSGKHVQFTCEG-----CKSPFKRSVRN-ITYSC 236
QY 70 LPKQPCDHFKNVYKTRHQRHHRKPNKHSRACQFLKQC 110
Db 237 RGRNCPID-----QHRNQCYCR-----LKXC 260

RESULT 9
CO1368 PRELIMINARY; PRT; 3190 AA.
AC CO1368;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CREB-binding protein homolog.
GN NEJ OR CG15319.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263578; PubMed=9109493;
RA Akimaru H., Chen Y., Dai P., Hou D.X., Nonaka M., Smolik S.M.,
RA Armstrong S., Goodman R.H., Ishii S.;
RT "Drosophila Cbp is a co-activator of cubitus interruptus in hedgehog
RT signalling."

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RL Nature 386:735-738 (1997).
DR EMBL; U88570; AAB3050.1; -.
DR TRANSFAC; T03236; -.
DR FlyBase; FBgn0015624; nej.
DR InterPro; IPR001487; Bromodomain.
DR InterPro; IPR003101; KIX.
DR InterPro; IPR000197; TAZ_finger.
DR InterPro; IPR000433; Znf_ZZ.
DR Pfam; PF00439; bromodomain; 1.
DR Pfam; PF02172; KIX; 1.
DR Pfam; PF02135; zf-TAZ; 2.
DR Pfam; PF00569; ZZ; 1.
DR PRINTS; PR00503; BROMODOMAIN.
DR SMART; SM0297; BROMO; 1.
DR SMART; SM00551; Znf_TAZ; 2.
DR SMART; SM00291; Znf_ZZ; 1.
DR PROSITE; PS00633; BROMODOMAIN_1; 1.
DR PROSITE; PS0014; BROMODOMAIN_2; 1.
DR PROSITE; PS00134; ZF_TAZ; 2.
DR PROSITE; PS01357; ZF_ZZ_1; 1.
DR PROSITE; PS0135; ZF_ZZ_2; 1.
DR PROSITE; PS0135; ZF_ZZ_2; 1.
SQ SEQUENCE 3190 AA; 331879 MW; E53526F78BC055A8 CRC64;

Query Match 11.0%; Score 71; DB 5; Length 3190;
Best Local Similarity 26.7%; Pred. No. 51;
Matches 23; Conservative 11; Mismatches 30; Indels 22; Gaps 3;

QY 25 NPGVARGHRDRGQASRRWLQEGGQCECKDWFLRAPRRKFTMTVSGLPKQPCDHFKNV 84
Db 2390 NPQEA-----RKQSIQRCIQSLAHACQCDANCRLP-----SCQMKLVV 2429
QY 85 KTRTHQRHHRKPNKHSRACQFLKQC 110
Db 2430 QHTKNCK--RKPNGGCPICKQLIALC 2453

RESULT 10
QW321 PRELIMINARY; PRT; 3276 AA.
ID QW321;
AC QW321;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG15319 protein.
GN NEJ OR CG15319.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Besu P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foutel C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

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CC Sordariales; Sordariaceae; Neurospora.
CX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Align V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.
RL Submitted (MAY-2000) to the ENBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora Genome project;
RL Submitted (NOV-2001) to the ENBL/GenBank/DBJ databases.
DR EMBL; AL356834; CAD11425.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1290 AA; 137768 MW; 1076A879259BEB70 CRC64;

Query Match 10.9%; Score 70.5; DB 3; Length 1290;
Best Local Similarity 24.5%; Pred. No. 23;
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

QY 33 RDRGQASRWLQEGQCECKDWFLRPRKFMVTS---GLPKKQCPDHFKNVKK--T 87
DQ 454 RNKKKKKKKKQEGSKGSK-----LRAPESAMPVSVVWSPSRANPLPRWQGHINGDV 508
DQ 88 RQHRHR-----KPKNSRACQF--LKQCQLRSFA 116
DQ 509 GHOSHQHMVMDGYVRLWSEKLEPH---QQFARLRKAEALALYA 550

RESULT 13
Q9BRN8 PRELIMINARY; PRT; 117 AA.
AC Q9BRN8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RC TISSUE=Eye;
RL Submitted (APR-2001) to the ENBL/GenBank/DBJ databases.
DR EMBL; BC06151; AA06151.1; -.
KW Hypothetical protein.
SQ SEQUENCE 117 AA; 13085 MW; 77A87C1DC40665DC CRC64;

Query Match 10.9%; Score 70; DB 4; Length 117;
Best Local Similarity 29.5%; Pred. No. 2.2;
Matches 26; Conservative 7; Mismatches 23; Indels 32; Gaps 5;

QY 16 LMSVSSSLNPGVAR---GHRDRGQASRWLQEGQCECKDWFLRPRKFMVTSGLPK 72
DQ 18 LLSMV-----EGPARPGSCWDPTQCTRTWL-----LSHTPRRW--ISGLPR 58
QY 73 KQCP-----CDHFKNVKKTRHQ 90
DQ 59 ASRLGEEPPPLPYCDQAYGEISIRHR 86

RESULT 14
Q97120 PRELIMINARY; PRT; 743 AA.
AC Q97120;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Retinoic acid receptor RXR.
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatoides; Schistosomatidae; Schistosoma.

CX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RA Freebern W.J., Oman A., Niles E.G., Christen L., Loverde P.T.;
RT "Identification of a cDNA encoding a retinoid X receptor homologue from Schistosoma mansoni. Evidence for a role in female-specific gene expression.";
RJ J. Biol. Chem. 274:4577-4585 (1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; AF094759; BA016119.1; -.
HSSP; P19793; IXXR.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Steroid_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PROSITE; PS00035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI_1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00047; STROIDFINGER.
DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription; Transcription regulation; Zinc; Zinc-finger.
KW SEQUENCE 743 AA; 82558 MW; 4CA9D287270B64DA CRC64;

Query Match 10.9%; Score 70; DB 5; Length 743;
Best Local Similarity 28.4%; Pred. No. 15;
Matches 29; Conservative 15; Mismatches 28; Indels 30; Gaps 7;

QY 18 SMVSSSLNP-GVARGHRDRGQASRWLQEGQCE-CKDWFLRPRKFMVTS---SGLPK 72
DQ 261 SVNTNLNPLVICGDKASKG-----HYGVISCEGCKGPKRTVKQLVYVCRBSG--- 311
QY 73 KQCP-----CDH-----PKGNVKKTRQHRHKKPKH 99
DQ 312 -QCPVDRRKRTRCQHCRCFQCLAKGMKKEAVQERHRPSSN 352

RESULT 15
Q9INJ0 PRELIMINARY; PRT; 746 AA.
AC Q9INJ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG11502-PA.
GN SVP.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RJ MEDLINE-2019606; PubMed-10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
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Search completed: January 29, 2004, 11:55:38
Job time : 36 secs

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöckes A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2183-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky F., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003695; AAN13541.1; .
SQ SEQUENCE 746 AA; 76814 MW; D6085838A848087B CRC64;

Query Match 10.9%; Score 70; DB 5; Length 746;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
QY 21 SSSLNPG-----VAGHRDRGQASRRWLQGGQCECKDQWFLRPRKFTVSG 69
Db 183 SQSSNSGSDSKQNICVVCVCGDKSKHYGQTCEG-----CKSFFKESVERN-LTYSC 235
QY 70 LPKQCCPDHFKGNVKKTRQHRHRKXKHSRACQOFLKQC 110
Db 237 RGRNRCPID-----QHRNQCCQYCR-----LKKC 260

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 29, 2004, 11:49:07 ; Search time 14 Seconds
(without alignments)
399.727 Million cell updates/sec

Title: US-09-786-260-1

Perfect score: 644

Sequence: 1 MKVLISLLLLPLMLMSV.....SPACQFLKQCLRSFALP 119

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	12.0	2269	1 RRPL_SV41	P35341 simian viru
2	74.5	11.6	448	1 VDR_COTJA	P49701 cuturnix co
3	74.5	11.6	451	1 VDR_CHICK	O42392 gallus gall
4	72.5	11.3	313	1 CLF3_RAT	O82778 rattus norv
5	71	11.0	411	1 SV44_BRARE	Q06725 brachydanio
6	71	11.0	1798	1 LMB2_HUMAN	P52268 homo sapien
7	71	11.0	2262	1 RRPL_P12HT	P36676 human parai
8	70	10.9	543	1 7UP1_DROME	P16375 drosophila
9	70	10.9	746	1 7UP2_DROME	P16376 drosophila
10	69.5	10.8	575	1 TRBM_HUMAN	P07204 homo sapien
11	69	10.7	314	1 SIX3_CHICK	O42406 gallus gall
12	68.5	10.6	422	1 VDR_MOUSE	P48281 mus musculu
13	68.5	10.6	422	1 VDR_XENLA	O13124 xenopus lae
14	68.5	10.6	423	1 VDR_RAT	P31053 rattus norv
15	68.5	10.6	424	1 VDR_BOVIN	Q28037 bos taurus
16	68.5	10.6	427	1 VDR_HUMAN	P11473 homo sapien
17	68.5	10.6	647	1 VE1_HPV40	P36727 human papil
18	67	10.4	376	1 CPB2_ARATH	Q91XW3 arabidopsis
19	67	10.4	475	1 HTM_BACSU	P42087 bacillus su
20	67	10.4	529	1 YB98_HUMAN	Q9ULM2 homo sapien
21	66.5	10.3	422	1 COT1_MOUSE	Q06632 mus musculu
22	66.5	10.3	423	1 COT1_MOUSE	P10589 homo sapien
23	66.5	10.3	424	1 COT1_BOVIN	Q9TTR8 bos taurus
24	66.5	10.3	3301	1 CLF3_MOUSE	Q1Z110 mus musculu
25	66	10.2	1339	1 SMCY_HUMAN	Q9BY66 homo sapien
26	65.5	10.2	646	1 VE1_HPV07	Q05133 human papil
27	65.5	10.2	706	1 FZD5_HUMAN	Q06353 homo sapien
28	65	10.1	363	1 PGL1_COLLN	Q00446 collettotric
29	65	10.1	441	1 COAT_SOCMV	P15627 soybean chl
30	64.5	10.0	534	1 Z397_HUMAN	Q8NF99 homo sapien
31	64.5	10.0	622	1 MAX_MOUSE	Q04853 mus musculu
32	64	9.9	227	1 ZN77_HUMAN	Q15935 homo sapien
33	64	9.9	246	1 SIX6_CHICK	Q93307 gallus gall

34	63.5	9.9	262	1 UT11_CAEL	Q09462 caenorhabdi
35	63.5	9.9	326	1 ZN73_HUMAN	O43830 homo sapien
36	63	9.8	160	1 ECP_PANTR	P47780 pan troglod
37	63	9.8	246	1 SIX6_HUMAN	O85475 homo sapien
38	63	9.8	246	1 SIX6_MOUSE	Q9GZ28 mus musculu
39	63	9.8	332	1 SIX3_HUMAN	O95343 homo sapien
40	63	9.8	333	1 SIX3_MOUSE	Q82233 mus musculu
41	63	9.8	371	1 RAL4_YEAST	P28519 saccharomyc
42	62.5	9.7	156	1 RNS7_HUMAN	Q9H1E1 homo sapien
43	62.5	9.7	410	1 COT2_CHICK	Q90733 gallus gall
44	62.5	9.7	414	1 COT2_BOVIN	Q9CTR7 bos taurus
45	62.5	9.7	414	1 COT2_HUMAN	P24468 homo sapien

ALIGNMENTS

RESULT 1
RRPL_SV41
ID RRPL_SV41 STANDARD; PRT; 2269 AA.
AC P35341;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE (L protein).
GN L.
OS Simian virus 41 (SV41).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Toshiba/Chanock;
RX MEDLINE=93019033; PubMed=1328485;
RA Kusagawa S., Komada H., Tsurudome M., Kawano M., Matsumura H.,
"Nucleotide sequence analysis of the simian virus 41 gene encoding
the large (L) protein and construction of a phylogenetic tree for the
L proteins of paramyxoviruses".
RT J. Gen. Virol. 73:2743-2750(1992).
RL - FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
CC SYNTHESIZE IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MENAS, RNA EDITING OF THE P
CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N).
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
CC
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X64275; CAA45569.1; -
CC PIR; JQ1750; JQ1750.
CC InterPro; IPR007098; RNA_pol_monon.
CC InterPro; IPR001016; Viral_RNA_pol_L.
CC Pfam; PF00946; Paramyx_RNA_pol_1.
CC Transferrase; RNA-directed RNA polymerase.
SQ SEQUENCE 2269 AA; 256429 MW; 3BD60C14AA161F5B CRC64;

Query Match 12.0%; Score 77; DB 1; Length 2269;
Best Local Similarity 27.5%; Pred. No. 4.7;
Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;

QY 13 PLMLMSVSSSLNPGVARGHRRGQAS-----RRWIQ-----EGGQECR--CK 53
DB 422 PLSLPGNASKSL-----TELHHDNSE-SYEYTLRHWKELSLIEFKKCFDFDGPGEISIFMK 477

QY 54 DWFLRPRKRWTVSGLPKQPCDHPKGNVKKTRHORHH-RKPNKHSR 101
Db 478 DKAIQAPKDWVS-----FKSLIKQHORHHHPNPNR 514

RESULT 2

ID VDR_COTJA STANDARD; PRT; 448 AA.
AC P49701;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR11.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC TISSUE=Chorioallantoic membrane;
RX MEDLINE=95062315; PubMed=792109;
RA Blarouesi M.A., Frahl J.M., Deluca H.F.;
RT "The avian vitamin D receptors: primary structures and their origins."
RT Proc. Natl. Acad. Sci. U.S.A. 91:11596-11600(1994).
CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative initiation;
CC Comment=2 isoforms, A (shown here) and B, are produced by alternative initiation;
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1 subfamily.
CC
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CC
CC EMBL; U12641; AAA56725.1; -.
CC PIR; I50451; I50451.
CC HSP; O75469; IILG.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Stdhrm_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PRINTS; PR000398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC Problem; P000035; Znf_C4steroid; 1.
CC DR SMAR1; SM00430; HOL1; 1.
CC DR SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Alternative initiation.
KW CHAIN 1 448 VITAMIN D3 RECEPTOR, ISOFORM A.
FT CHAIN 26 448 FOR ISOFORM B.
FT INIT MET 26 26
FT DNA_BIND 44 109 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 44 64 C4-TYPE.
FT ZN_FING 80 104 C4-TYPE.
FT DOMAIN 110 212 HINGE.
FT DOMAIN 213 448 LIGAND-BINDING.
SQ SEQUENCE 448 AA; 50668 MW; FCF1FC3DEAEAF3E CRC64;

Query Match 11.6%; Score 74.5; DB 1; Length 448;
Best Local Similarity 32.9%; Pred. No. 1.8;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;
QY 50 CE-CKDWFLRPRKRWTVSGLPKQPCDHPKGNVKKTRHORHH-RKPNKHSRACQQLK 108
Db 61 CECKGFFRRSMKRWKAMFT-----CP---FSGCKITKDNR-----RHQACR--LK 102

QY 109 QC---QLRSFAL 117

Db 103 RCVDIGMKKEFIL 115

RESULT 3

ID VDR_CHICK STANDARD; PRT; 451 AA.
AC O42392;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR11.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
RC STRAIN=Leghorn; TISSUE=Kidney;
RX MEDLINE=97223369; PubMed=9056239;
RA Lu Z., Hanson K., Deluca H.F.;
RT "Cloning and origin of the two forms of chicken vitamin D receptor."
RT Arch. Biochem. Biophys. 339:99-106(1997).
RN [2]
RP SEQUENCE OF 45-114 FROM N.A.
RX MEDLINE=87149040; PubMed=3029866;
RA McDonnell D.P., Mangelsdorf D.J., Pike J.W., Haussler M.R.,
RA O'Malley B.W.;
RT "Molecular cloning of complementary DNA encoding the avian receptor for vitamin D."
RT Science 235:1214-1217(1987).
CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative initiation;
CC Comment=2 isoforms, A (shown here) and B, are produced by alternative initiation;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND INTESTINE.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1 subfamily.
CC
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CC
CC EMBL; AF011356; AAB62579.1; -.
CC PIR; A60912; A60912.
CC HSP; O75463; IILG.
CC TRANSFAC; T00884; -.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Stdhrm_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.

DR PRINTS; PRO0047; STROIDFINGER.
 DR PRODOM; ED000035; Znf_C4steroid; 1.
 DR SMART; SM00430; Znf_C4; 1.
 DR PROSITE; PS00399; Znf_C4; 1.
 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1.
 KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 Zinc-finger; Alternative initiation.
 FT CHAIN 1 451 VITAMIN D3 RECEPTOR, ISOFORM A.
 FT INIT_NET 15 451 FOR ISOFORM B.
 FT ZN_BIND 47 112 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 47 67 C4-TYPE.
 FT ZN_FING 83 107 C4-TYPE.
 FT DOMAIN 113 215 HINGE.
 FT DOMAIN 216 451 LIGAND-BINDING.
 SQ SEQUENCE 451 AA; 51299 MW; 2078B6AC8D855FC CRC64;
 Query Match 11.6%; Score 74.5; DB 1; Length 451;
 Best Local Similarity 32.9%; Pred. No. 1.8;
 Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;
 QY 50 CE-CKDFELRPRKEMTYSGLPKQPCDHPKGNVKTQRHHRKPKHSRACQQLX 108
 DB 64 CECKGFFRSMRKAMFT-----CP---FNGDKITKDNR-----RHQACR--LX 105
 QY 109 QC---QLRSFAL 117
 DB 106 RCVDIGMWKEFIL 118
 RESULT 4
 CLIR3 RAT STANDARD; PRT; 3313 AA.
 AC 088278;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cadherin EGF LAG seven-pass G-type receptor 3 precursor (Multiple
 DE epidermal growth factor-like domains 2).
 GN CELSR3 OR MECP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98360089; PubMed=9693030;
 RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
 RT "Identification of high-molecular-weight proteins with multiple
 RT EGF-like motifs by motif-trap screening.";
 RL Genomics 51:27-34(1998).
 CC -!- FUNCTION: Receptor that may have an important role in cell/cell
 CC signaling during nervous system formation.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the brain. Expressed in
 CC cerebellum, olfactory bulb, cerebral cortex, hippocampus and
 CC brain stem.
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -!- SIMILARITY: Contains 9 cadherin domains.
 CC -!- SIMILARITY: Contains 8 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 laminin G-like domains.
 CC -!- SIMILARITY: Contains 1 laminin EGF-like domain.
 CC -!- SIMILARITY: Contains 1 GPS domain.
 CC -----
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DR EMBL; AB011528; BAA32459.1; -.
 DR HSSP; P00740; 1EDM.
 DR InterPro; IPR00152; Asx hydroxyl.
 DR InterPro; IPR002126; Cadherin.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR00832; GPCR secretin.
 DR InterPro; IPR001879; hormn_receptor.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002049; Laminin EGF.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR000203; PKD_cys-rich.
 DR Pfam; PF00002; 7tm 2; 1.
 DR Pfam; PF00028; cadherin; 9.
 DR Pfam; PF00008; EGF; 6.
 DR Pfam; PF01825; GFS; 1.
 DR Pfam; PF02793; HRM; 1.
 DR Pfam; PF00054; laminin G; 1.
 DR PRINTS; PRO0205; CADHERIN.
 DR PRINTS; PRO0011; EGF-LAMININ.
 DR PRINTS; PRO0249; GPCRSECRETIN.
 DR SMART; SM00112; CA; 9.
 DR SMART; SM00181; EGF; 6.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00008; Hormr; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX HYDROXYL; 1.
 DR PROSITE; PS00232; CADHERIN 1; 7.
 DR PROSITE; PS00268; CADHERIN 2; 8.
 DR PROSITE; PS00022; EGF 1; 6.
 DR PROSITE; PS01186; EGF 2; 4.
 DR PROSITE; PS00221; GPS; 1.
 DR PROSITE; PS00025; LAM G DOMAIN; 2.
 DR PROSITE; PS00649; G-PROTEIN RECF_F2_1; FALSE_NEG.
 DR PROSITE; PS00550; G-PROTEIN RECF_F2_2; FALSE_NEG.
 DR PROSITE; PS00227; G-PROTEIN RECF_F2_3; 1.
 DR PROSITE; PS00261; G-PROTEIN RECF_F2_4; 1.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
 KW Developmental protein; Hydroxylation; Signal.
 FT SIGNAL 1 31 POTENTIAL EGF LAG SEVEN-PASS G-TYPE
 FT CHAIN 32 3313 RECEPTOR 3.
 FT DOMAIN 32 2538 CADHERIN EGF LAG SEVEN-PASS G-TYPE
 FT TRANSMEM 2539 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 2560 1 (POTENTIAL).
 FT TRANSMEM 2571 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 2591 2 (POTENTIAL).
 FT TRANSMEM 2592 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 2600 3 (POTENTIAL).
 FT TRANSMEM 2621 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 2642 4 (POTENTIAL).
 FT TRANSMEM 2663 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 2680 5 (POTENTIAL).
 FT TRANSMEM 2701 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 2724 6 (POTENTIAL).
 FT TRANSMEM 2725 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 2746 7 (POTENTIAL).
 FT TRANSMEM 2753 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 2774 3313 CADHERIN 1.
 FT TRANSMEM 317 424 CADHERIN 2.
 FT DOMAIN 425 536 CADHERIN 3.
 FT TRANSMEM 537 642 CADHERIN 4.
 FT DOMAIN 643 747 CADHERIN 5.
 FT TRANSMEM 748 849 CADHERIN 6.
 FT DOMAIN 850 952 CADHERIN 7.
 FT TRANSMEM 953 1058 CADHERIN 8.
 FT DOMAIN 1059 1160 CADHERIN 9.
 FT TRANSMEM 1066 1257 EGF-LIKE 1.
 FT DOMAIN 1366 1424 EGF-LIKE 2.
 FT TRANSMEM 1426 1462 EGF-LIKE 3.
 FT DOMAIN 1466 1505 LAMININ G-LIKE 1.
 FT TRANSMEM 1506 1710

```

DE  Steroid receptor homolog SVP 44.
OS  Brachydanio rerio (Zebrafish) (Danio rerio).
GN  SVF24 OR NR2P1.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC  Cyprinidae; Danio.
NCBI_TaxID=7955;
RN  [1]
RS  SEQUENCE FROM N.A.
RR  MEDLINE=93223680; PubMed=8467797;
RX  FJose A., Nornes S., Weber U., Mlodzik M.;
RA  "Functional conservation of vertebrate seven-up related genes in
RT  neurogenesis and eye development.";
RL  EMBO J. 12:1403-1414(1993).
CC  -1- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
CC  CELLS PRECURSORS DURING EYE DEVELOPMENT.
CC  -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC  -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC  subfamily.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X70299; CAA49780.1; -.
DR  PIR; S35333; S35333.
DR  HSSP; P19793; 2NLL.
DR  ZFIN; ZDB-GENE-980526-115; nr2f1.
DR  InterPro; IPR000536; Hormone_rec_lig.
DR  InterPro; IPR001723; Steroid_receptor.
DR  InterPro; IPR001628; Znfc4steroid.
DR  Pfam; PF00104; hormone_rec; 1.
DR  Pfam; PF00105; zf-C4; 1.
DR  PRINTS; PR00398; STRDHORMONER.
DR  PRINTS; PR00047; STROIDFINGER.
DR  ProDom; PD000035; Znfc4steroid; 1.
DR  SMART; SM00430; HOLI_1.
DR  SMART; SM00399; Znfc4; 1.
DR  PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR  Receptor; Transcription regulation; DNA-binding; Nuclear protein;
DR  Zinc-finger; Vision.
FT  DNA_BIND 76 141 NUCLEAR RECEPTOR-TYPE.
FT  ZN_FING 76 96 C4-TYPE.
FT  ZN_FING 112 136 C4-TYPE.
FT  SEQUENCE 411 AA; 45482 MW; B0405FE4AEFA0202 CRC64;
SQ
Query Match 11.0%; Score 71; DB 1; Length 411;
Best Local Similarity 26.3%; Pred. No. 3.8;
Matches 26; Conservative 14; Mismatches 27; Indels 32; Gaps 6;

QY 26 PGVA -RGHRDRQASRR-----WLQEGQCE-CXKWFRLPRKFMVTSGLP 71
DB 56 PTAGDKGSONSQSOHTECVCGDKSGKHGYQFTCEGCKSFKEVSVERN-LTYTCRA 114
QY 72 KKQCPDHFKNVKKTRHORHHRKPKHSRACQQFLKQC 110
DB 115 NRCNCPID-----OHRNQCQYCR-----LKKC 136

RESULT 6
ID LMB2 HUMAN STANDARD; PRT; 1798 AA.
AC P55268; O16321;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (Laminin B1s chain).
DE LMB2 OR LAMS.
OS Homo sapiens (human)

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]_TaxID=9506;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95213013; PubMed=7698745;
 RA Wewer U.M., Gerscke D.R., Durkin M.E., Kurtz K.S., Mattei M.-G.,
 RT Champlaud M.F., Burgeson R.E., Albrechtsen R.;
 RT "Human beta 2 chain of laminin (formerly S chain): cDNA cloning,
 RL chromosomal localization, and expression in carcinomas.";
 RN Genomics 24:243-252(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95316263; PubMed=7795887;
 RA Iivanainen A., Vuolteenaho R., Sainio K., Eddy R., Shows T.B.,
 RT Sariola H., Trygvsen K.;
 RT "The human laminin beta 2 chain (S-laminin): structure, expression in
 RL fetal tissues and chromosomal assignment of the LAMB2 gene.";
 CC Matrix Biol. 14:489-497(1995).
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration, and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end.
 CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
 CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC
 CC CLEFT OF THE NEUROMUSCULAR JUNCTION.
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
 CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -!- SIMILARITY: Contains 13 laminin EGF-like domains.
 CC -!- SIMILARITY: Contains 1 laminin IV domain.
 CC -----
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 CC -----
 DR EMBL; Z68155; CAA92279.1; -.
 DR EMBL; Z68156; CAA92279.1; JOINED.
 DR EMBL; X79683; CAA56130.1; -.
 DR EMBL; S77512; AAB34682.2; -.
 DR PIR; S53869; S53869.
 DR HSSP; P02468; IKLO.
 DR Genew; HGNC:6487; LAMB2.
 DR MIN; I50325; -.
 DR GO; GO:0005605; C:basal lamina; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR002045; Laminin_EGF.
 DR InterPro; IPR001886; LamN.
 DR Pfam; PF00053; laminin EGF; 13.
 DR Pfam; PF00055; laminin Nterm; 1.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR SMART; SM00180; EGF Lam; 13.
 DR SMART; SM00136; LamN; 1.
 DR PROSITE; PS00022; EGF 1; 10.
 DR PROSITE; PS01156; EGF 2; 2.
 DR PROSITE; PS01249; LAMININ TYPE EGF; 12.
 KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 RN Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 1798 LAMININ BETA-2 CHAIN.
 FT
 FT DOMAIN 33 280 LAMININ N-TERMINAL (DOMAIN VI).
 FT DOMAIN 283 346 LAMININ EGF-LIKE 1.
 FT DOMAIN 347 409 LAMININ EGF-LIKE 2.
 FT DOMAIN 410 469 LAMININ EGF-LIKE 3.
 FT DOMAIN 470 521 LAMININ EGF-LIKE 4.
 FT DOMAIN 522 552 LAMININ EGF-LIKE 5 (INCOMPLETE).
 FT DOMAIN 553 781 LAMININ DOMAIN IV.
 FT DOMAIN 783 830 LAMININ EGF-LIKE 6.
 FT DOMAIN 831 876 LAMININ EGF-LIKE 7.
 FT DOMAIN 877 927 LAMININ EGF-LIKE 8.
 FT DOMAIN 927 985 LAMININ EGF-LIKE 9.
 FT DOMAIN 986 1037 LAMININ EGF-LIKE 10.
 FT DOMAIN 1038 1094 LAMININ EGF-LIKE 11.
 FT DOMAIN 1095 1142 LAMININ EGF-LIKE 12.
 FT DOMAIN 1143 1189 LAMININ EGF-LIKE 13.
 FT DOMAIN 1190 1442 DOMAIN ALPHA.
 FT DOMAIN 1443 1798 DOMAIN I.
 FT DOMAIN 1253 1319 COILED COIL (POTENTIAL).
 FT DOMAIN 1472 1526 COILED COIL (POTENTIAL).
 FT DOMAIN 1577 1790 COILED COIL (POTENTIAL).
 FT DISULFID 283 292 BY SIMILARITY.
 FT DISULFID 285 310 BY SIMILARITY.
 FT DISULFID 312 321 BY SIMILARITY.
 FT DISULFID 324 344 BY SIMILARITY.
 FT DISULFID 347 356 BY SIMILARITY.
 FT DISULFID 349 374 BY SIMILARITY.
 FT DISULFID 377 386 BY SIMILARITY.
 FT DISULFID 389 407 BY SIMILARITY.
 FT DISULFID 410 423 BY SIMILARITY.
 FT DISULFID 412 438 BY SIMILARITY.
 FT DISULFID 440 449 BY SIMILARITY.
 FT DISULFID 452 467 BY SIMILARITY.
 FT DISULFID 470 484 BY SIMILARITY.
 FT DISULFID 472 491 BY SIMILARITY.
 FT DISULFID 493 502 BY SIMILARITY.
 FT DISULFID 505 519 BY SIMILARITY.
 FT DISULFID 783 795 BY SIMILARITY.
 FT DISULFID 785 802 BY SIMILARITY.
 FT DISULFID 804 813 BY SIMILARITY.
 FT DISULFID 816 828 BY SIMILARITY.
 FT DISULFID 831 843 BY SIMILARITY.
 FT DISULFID 833 850 BY SIMILARITY.
 FT DISULFID 852 861 BY SIMILARITY.
 FT DISULFID 864 874 BY SIMILARITY.
 FT DISULFID 877 886 BY SIMILARITY.
 FT DISULFID 879 893 BY SIMILARITY.
 FT DISULFID 896 905 BY SIMILARITY.
 FT DISULFID 908 924 BY SIMILARITY.
 FT DISULFID 927 943 BY SIMILARITY.
 FT DISULFID 929 954 BY SIMILARITY.
 FT DISULFID 956 965 BY SIMILARITY.
 FT DISULFID 968 983 BY SIMILARITY.
 FT DISULFID 986 1000 BY SIMILARITY.
 FT DISULFID 988 1007 BY SIMILARITY.
 FT DISULFID 1010 1019 BY SIMILARITY.
 FT DISULFID 1022 1035 BY SIMILARITY.
 FT DISULFID 1035 1095 BY SIMILARITY.
 FT DISULFID 1097 1114 BY SIMILARITY.
 FT DISULFID 1116 1125 BY SIMILARITY.
 FT DISULFID 1128 1140 BY SIMILARITY.
 FT DISULFID 1143 1155 BY SIMILARITY.
 FT DISULFID 1145 1162 BY SIMILARITY.
 FT DISULFID 1164 1173 BY SIMILARITY.
 FT DISULFID 1176 1187 BY SIMILARITY.
 FT DISULFID 1190 1190 INTERCHAIN (PROBABLE).
 FT DISULFID 1193 1193 INTERCHAIN (PROBABLE).
 FT DISULFID 1797 1797 INTERCHAIN (PROBABLE).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 1095 1095 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 1249 1249 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 1308 1308 N-LINKED (GLCNAC. . .)

FT CARBOHYD 1348 1348 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1499 1499 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 914 914 R -> G (IN REF. 2).
 FT CONFLICT 1179 1179 G -> A (IN REF. 2).
 SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;
 Query Match 11.0%; Score 71; DB 1; Length 1798;
 Best Local Similarity 28.4%; Pred. No. 16;
 Matches 27; Conservative 6; Mismatches 46; Indels 16; Gaps 4;
 QY 23 SLNPGVARGHDDR-----GQASRWLQEGGQCE-CKDWFLRAPRRKFTVSLGPKKQCF 76
 DB 873 SCRPCVNGHADENHTHTGACLRGDRDTGGEHCERCIAAGFHRDPRILFY-----GGQCRPCF 928
 QY 77 CDHFKGNVKKTRHQRHHRKPNKHSRACQQLKQCC 111
 DB 929 CPEGFGS-----QRHFTATSCHQDEYSQIVCHCR 957
 RESULT 7
 RRPL_P12HT
 ID RRPL_P12HT STANDARD; PRT; 2262 AA.
 AC P26676;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein).
 GN L.
 OS Human parainfluenza 2 virus (strain Toshiba) (PIV-2).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
 OX NCBI_TaxID=11214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91252221; PubMed=1645865;
 RA Kawano M., Okamoto K., Bando H., Tsurudome M., Komada H.,
 RA Nishio M., Ito Y.;
 RT "Characterizations of the human parainfluenza type 2 virus gene
 RT encoding the L protein and the intergenic sequences.";
 RL Nucleic Acids Res. 19:2739-2746(1991).
 CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
 CC SYNTHESIZE IN RNA SYNTHESIS, CAPING, METHYLATION AND POLY(A)
 CC SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs, RNA EDITING OF THE P
 CC GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
 CC
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 CC
 CC EMBL; X57559; CAA40788.1; -;
 CC PIR; S16664; S16664.
 CC InterPro; IPR007098; RNA pol monon.
 CC InterPro; IPR001016; Viral RNA pol.L.
 CC Pfam; PF00946; Paramyx_RNA_pol; 1.
 KW Transfrase; RNA-directed RNA polymerase.
 SQ SEQUENCE 2262 AA; 256380 MW; 82469303F4453B48 CRC64;
 Query Match 11.0%; Score 71; DB 1; Length 2262;
 Best Local Similarity 26.6%; Pred. No. 20;
 Matches 29; Conservative 13; Mismatches 31; Indels 36; Gaps 6;
 QY 13 PLMLNSMYSLSLPGVARGHDDQAS-----RWLQ-----EGQCE--CX 53
 DB 421 PLILPKNASKSL-----IEFQDNAEISYEYTLKHWKEISLIEFRKCFDFDPEELSPMK 476

OY 54 DWFLRAPRRKFTVSLGPKKQCPDHFKNVKKTRHQRH-RKPNKHSR 101
 DB 477 DKAIAPRSDWMSV-----FRSLIKQRHHPMPAPFNR 513
 RESULT 8
 7UP1_DROME
 ID 7UP1_DROME STANDARD; PRT; 543 AA.
 AC P16375; OVG80;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Steroid receptor seven-up type 1.
 GN SVP OR NR2F3 OR CG11502.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90124631; PubMed=2105156;
 RA Mlodzik M., Hiroi Y., Weber U., Goodman C.S., Rubin G.M.;
 RT "The Drosophila seven-up gene, a member of the steroid receptor gene
 RT superfamily, controls photoreceptor cell fates.";
 RL Cell 60:211-224(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Clawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.N., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Stirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J., Yang Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
 CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

```
CC Name=Type 1;
CC IsoId=p16375-1; Sequence=Displayed;
CC Name=Type 2;
CC IsoId=p16376-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC -----
CC EMBL; M28863; AAA62770.1; -
CC EMBL; AE003695; AAP54773.1; -
CC PIR; A32893; A32693.
CC HSSP; P19793; 2NLL.
CC TRANSFAC; T02741; -
CC FLYbase; FBgn0003651; svp.
CC GO; GO:0005737; C:cardioblast cell fate determination; IEP.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001628; Stdhrmn_receptor.
CC Pfam; PF00104; hormone_rec; 1.
CC PRINTS; PR00047; STROIDFINGER.
CC PRODOM; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Vision; Alternative splicing.
CC DNA BIND 200 265 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 200 220 C4-TYPE.
CC ZN_FING 236 260 C4-TYPE.
CC ZN_SEQUENCE 543 AA; 57987 MW; 0BC189DCFLA27213 CRC64;
CC -----
CC Query Match 10.9%; Score 70; DB 1; Length 543;
CC Best Local Similarity 26.7%; Pred. No. 6.4;
CC Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
CC -----
CC QY 21 SSSLNPG-----VARGHRDRGQASRWLQGGQCECKQWFLRAPRRKFTVSG 69
CC Db 183 SOSNSGSGQIDSKQNIETCVCGDKSSGKHGQFTCEG-----CKSFFKRSVRRN-LTYSC 236
CC QY 70 LPKQPCDHFHKGNYKTRHORHHRKPNKHSRACQFLKQC 110
CC Db 237 RGSRCNPID-----QHRNQCYCR-----LKKC 260
CC -----
CC RESULT 9
CC TUP2 DROME
CC ID TUP2 DROME STANDARD; PRT; 746 AA.
CC AC P16376;
CC DT 01-AUG-1990 (Rel. 15, Created)
CC DT 01-NOV-1990 (Rel. 16, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Steroid receptor seven-up type 2.
CC GN SVP OR NR2F3.
CC OS Drosophila melanogaster (fruit fly).
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC OC Ephydroidea; Drosophilidae; Drosophila.
CC OX NCBI_TaxID=7227;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RP MEDLINE=90124631; PubMed=2105166;
CC RX Mlodzik M., Hiromi Y., Weber U., Goodman C.S., Rubin G.M.;
CC RA
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```
RT "The Drosophila seven-up gene, a member of the steroid receptor gene
RT superfamily, controls photoreceptor cell fates.";
RL Cell 60:211-224(1990).
CC -!- FUNCTION: PUTATIVE RECEPTOR THAT IS REQUIRED IN PHOTORECEPTOR
CC CELLS PRECURSORS DURING EYE DEVELOPMENT.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Type 2; Sequence=Displayed;
CC IsoId=p16376-1; Sequence=Displayed;
CC Name=Type 1;
CC IsoId=p16375-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF NEURAL PRECURSORS.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR2
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M28864; AAA03014.1; -
CC PIR; B32693; B32693.
CC HSSP; P19793; 2NLL.
CC FLYbase; FBgn0003651; svp.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Stdhrmn_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC PRODOM; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOL1; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Vision; Alternative splicing.
CC DNA BIND 200 265 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 200 220 C4-TYPE.
CC ZN_FING 236 260 C4-TYPE.
CC ZN_SEQUENCE 746 AA; 76830 MW; 7F256AFD4165326D CRC64;
CC -----
CC Query Match 10.9%; Score 70; DB 1; Length 746;
CC Best Local Similarity 26.7%; Pred. No. 8.6;
CC Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;
CC -----
CC QY 21 SSSLNPG-----VARGHRDRGQASRWLQGGQCECKQWFLRAPRRKFTVSG 69
CC Db 183 SOSNSGSGQIDSKQNIETCVCGDKSSGKHGQFTCEG-----CKSFFKRSVRRN-LTYSC 236
CC QY 70 LPKQPCDHFHKGNYKTRHORHHRKPNKHSRACQFLKQC 110
CC Db 237 RGSRCNPID-----QHRNQCYCR-----LKKC 260
CC -----
CC RESULT 10
CC TREM HUMAN
CC ID TREM HUMAN STANDARD; PRT; 575 AA.
CC AC P07204;
CC DT 01-APR-1988 (Rel. 07, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Thrombomodulin precursor (Fetomodulin) (TM) (CD141 antigen).
CC GN THBD OR TREM.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
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RP SEQUENCE FROM N.A.
RX MEDLINE=86004395; PubMed=2820710;
RA Suzuki K., Kusumoto H., Deyashiki Y., Nishioka J., Maruyama I.,
RT Zushi M., Kawahara S., Honda G., Yamamoto S., Horiguchi S.;
RA "Structure and expression of human thrombomodulin, a thrombin
RT receptor on endothelium acting as a cofactor for protein C
RT activation.";
RL EMBO J. 6:1891-1897(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88024950; PubMed=2822087;
RA Wen D., Dittman W.A., Ye R.D., Deaven L.L., Majerus P.W., Sadler J.E.;
RT "Human thrombomodulin: complete cDNA sequence and chromosome
RT localization of the gene.";
RL Biochemistry 26:4350-4357(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87317665; PubMed=2819876;
RA Jackman R.W., Beiler D.L., Fritze L., Soff G., Rosenberg R.D.;
RT "Human thrombomodulin gene is intron depleted: nucleic acid sequences
RT of the cDNA and gene predict protein structure and suggest sites of
RT regulatory control.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6425-6429(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227801; PubMed=2836377;
RA Shirai T., Shiojiri S., Ito H., Yamamoto S., Kusumoto H.,
RA Deyashiki Y., Maruyama I., Suzuki K.;
RT "Gene structure of human thrombomodulin, a cofactor for thrombin-
RT catalyzed activation of protein C.";
RL J. Biochem. 103:281-285(1988).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227801; PubMed=2836377;
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Poel C.L., Toth B.J., Yi O., Nickerson D.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Delucas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almedia J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill M.D., Butler A.P., Carder C., Carter N.P., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Dunn M.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay X.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rameay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.B., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.W., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE SER-492, AND MUTAGENESIS.
RX MEDLINE=94029900; PubMed=8216207;
RA Gerleitz B., Hassell T., Vlahos C.J., Parkinson J.F., Bang N.U.,
RA Grinnell B.W.;
RT "Identification of the predominant glycosaminoglycan-attachment site
RT in soluble recombinant human thrombomodulin: potential regulation of

RT functional by glycosyltransferase competition for serine474.";
RL Biochem. J. 295:131-140(1993).
RN [8]
RP STRUCTURE BY NMR OF 389-407.
RX MEDLINE=96007474; PubMed=7559494;
RA Adler M., Sato M.H., Nitecki D.E., Lin J.H., Light D.R., Morser J.;
RT "The structure of a 19-residue fragment from the C-loop of the fourth
RT epidermal growth factor-like domain of thrombomodulin.";
RL J. Biol. Chem. 270:23366-23372(1995).
RN [9]
RP STRUCTURE BY NMR OF 364-407.
RX MEDLINE=96100636; PubMed=8528067;
RA Meiningner D.P., Hunter M.J., Komives E.A.;
RT "Synthesis, activity, and preliminary structure of the fourth
RT EGF-like domain of thrombomodulin.";
RL Protein Sci. 4:1683-1695(1995).
RN [10]
RP STRUCTURE BY NMR OF 427-444.
RX MEDLINE=95034791; PubMed=7947765;
RA Srinivasan J., Hu S., Hrabal R., Zhu Y., Komives E.A., Ni F.;
RT "Thrombin-bound structure of an EGF subdomain from human
RT thrombomodulin determined by transferred nuclear Overhauser
RT effects.";
RL Biochemistry 33:13553-13560(1994).
RN [11]
RP STRUCTURE BY NMR OF 427-444.
RX MEDLINE=96276211; PubMed=8745396;
RA Hrabal R., Komives E.A., Ni F.;
RT "Structural resiliency of an EGF-like subdomain bound to its target
RT protein, thrombin.";
RL Protein Sci. 5:195-203(1996).
RN [12]
RP STRUCTURE BY NMR OF 405-444.
RX MEDLINE=98035729; PubMed=9367781;
RA Sampoli Benitez B.A., Hunter M.J., Meiningner D.P., Komives E.A.;
RT "Structure of the fifth EGF-like domain of thrombomodulin: an
RT EGF-like domain with a novel disulfide-bonding pattern.";
RL J. Mol. Biol. 273:913-926(1997).
RN [13]
RP VARIANT TED TYR-486.
RX MEDLINE=95111115; PubMed=7811989;
RA Oehlin A.-K., Marlar R.A.;
RT "The first mutation identified in the thrombomodulin gene in a
RT 45-year-old man presenting with thromboembolic disease.";
RL Blood 85:330-336(1995).
RN [14]
RP VARIANT TED TYR-486, AND VARIANTS THR-43; ALA-79; SER-495 AND LEU-501.
RX MEDLINE=97341986; PubMed=9198186;
RA Oehlin A.-K., Norlund L., Marlar R.A.;
RT "Thrombomodulin gene variations and thromboembolic disease.";
RL Thromb. Haemost. 78:396-400(1997).
RN [15]
RP VARIANT VAL-473.
RX MEDLINE=97206518; PubMed=9157575;
RA Norlund L., Holm J., Zoller B., Oehlin A.-K.;
RT "A common thrombomodulin amino acid dimorphism is associated with
RT myocardial infarction.";
RL Thromb. Haemost. 77:248-251(1997).
RN [16]
RP VARIANT THR-43.
RX MEDLINE=99057299; PubMed=9843165;
RA Doggen C.J.M., Kunz G., Rosendaal F.R., Lane D.A., Vos H.L.,
RA Stubbs P.J., Manger Cats V., Ireland H.;
RT "A mutation in the thrombomodulin gene, 127G to A coding for Ala25Thr,
RT and the risk of myocardial infarction in men.";
RL Thromb. Haemost. 80:743-748(1998).
RN [17]
RP VARIANT VAL-473.
RX MEDLINE=21143723; PubMed=11245641;
RA Wu K.K., Aleksic N., Ahn C., Boerwinkle E., Folsom A.R.,
RA Juneja H.;
RT "Thrombomodulin Ala455Val polymorphism and risk of coronary heart
RT disease.";


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CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC
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CC
CC ENBL; D31969; BAA06737.1; -.
CC PIR; PC4019; PC4019.
CC HSP; P03372; IHQO.
CC TRANSFAC; T00883; -.
CC MGD; MGI:103076; Vdr.
CC GO; GO:0006874; P:calcium ion homeostasis; IMP.
CC GO; GO:0007275; P:development; IMP.
CC GO; GO:0001501; P:skeletal development; IMP.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Steroid_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Phosphorylation.
CC DNA BIND 24 89 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 24 44 C4-TYPE.
CC ZN_FING 60 84 C4-TYPE.
CC FT DOMAIN 90 186 HINGE.
CC FT DOMAIN 187 422 LIGAND-BINDING.
CC SEQUENCE 422 AA; 47851 MW; 4704CC8172445732 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLLAPRRKFTVSGLPKQCPCDHFPGKGVKTKTRHQRHRRKPNKHSRACQQLK 108
Db 41 CEGCKGFFRRSMKRAFT-----CP---FNGDCRITKDNR-----RHCQACR--LK 82

QY 109 QC-----QLRSFAL 117
Db 83 RCVDIGMKKEFIL 95

RESULT 13
ID_VDR_XENLA STANDARD; PRT; 422 AA.
AC Q13124;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR11.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Kidney;
RX MEDLINE=97307679; PubMed=9165021;

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RA Li Y.C., Bergwitz C., Jueppner H., Demay M.B.;
RT "Cloning and characterization of the vitamin D receptor from Xenopus
RL laevis."
RL Endocrinology 138:2347-2353(1997).
CC -!- FUNCTION: VDR MEDIATES THE ACTION OF VITAMIN D3 BY CONTROLLING
CC THE EXPRESSION OF HORMONE SENSITIVE GENES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: DETECTED IN ALL THE TISSUE EXAMINED. HIGHEST
CC LEVEL IN SMALL INTESTINE AND SKIN.
CC -!- DEVELOPMENTAL STAGE: FIRST DETECTED AT STAGE 13. INCREASES
CC GRADUALLY AND PEAKS AT STAGE 57-61 THEN DECREASES TO THE LEVEL
CC SEEN IN ADULT.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC ENBL; U91846; AAB58585.1; -.
CC HSP; O75469; 11LG.
CC InterPro; IPR000536; Hormone_rec_lig.
CC InterPro; IPR001723; Steroid_receptor.
CC InterPro; IPR001628; Znf_C4steroid.
CC Pfam; PF00104; hormone_rec; 1.
CC Pfam; PF00105; zf-C4; 1.
CC PRINTS; PR00398; STRDHORMONER.
CC PRINTS; PR00047; STROIDFINGER.
CC ProDom; PD000035; Znf_C4steroid; 1.
CC SMART; SM00430; HOLI; 1.
CC SMART; SM00399; Znf_C4; 1.
CC PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
CC DNA BIND 25 90 NUCLEAR RECEPTOR-TYPE.
CC ZN_FING 25 45 C4-TYPE.
CC ZN_FING 61 85 C4-TYPE.
CC FT DOMAIN 91 188 HINGE.
CC FT DOMAIN 189 422 LIGAND-BINDING.
CC SEQUENCE 422 AA; 48188 MW; C8A9F25414FEE9D5 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 422;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLLAPRRKFTVSGLPKQCPCDHFPGKGVKTKTRHQRHRRKPNKHSRACQQLK 108
Db 42 CEGCKGFFRRSMKRAFT-----CP---FNGDCRITKDNR-----RHCQSCR--LK 83

QY 109 QC-----QLRSFAL 117
Db 84 RCVDIGMKKEFIL 96

RESULT 14
ID_VDR_RAT STANDARD; PRT; 423 AA.
AC P13053;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR11.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

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RN RP SEQUENCE FROM N.A.
RX MEDLINE=89071726; PubMed=2849110;
RA Burmester J.K., Wiese R.J., Maeda N., Deluca H.;
RT "Structure and regulation of the rat 1,25-dihydroxyvitamin D3
RL receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 85:9499-9502(1988).
RN RP
RN RP SEQUENCE OF 58-423 FROM N.A.
RX MEDLINE=88124963; PubMed=2829212;
RA Burmester J.K., Maeda N., Deluca H.F.;
RT "Isolation and expression of rat 1,25-dihydroxyvitamin D3 receptor
RL cDNA."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1005-1009(1988).
RN RP
RN RP INTERACTION NCOA6.
RX MEDLINE=20325329; PubMed=10866662;
RA Mahajan M.A., Samuels H.H.;
RT "A new family of nuclear receptor coregulators that integrates nuclear
RL receptor signaling through CBP."
RL Mol. Cell. Biol. 20:5048-5063(2000).
RN RP
CC -|- FUNCTION: Nuclear hormone receptor. VDR mediates the action of
CC vitamin D3 by controlling the expression of hormone sensitive
CC genes.
CC -|- SUBUNIT: Interacts with NCOA3 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes.
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC
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CC
CC EMBL; J04147; AAA41089.1; -.
CC F01; A31761; A31761.
CC DR HSSP; P03372; LHCQ.
CC DR TRANSFAC; T00882; -.
CC DR InterPro; IPR000536; Hormone_rec_lig.
CC DR InterPro; IPR001723; Stdhnm_receptor.
CC DR InterPro; IPR001628; Znfc_Casteroid.
CC DR Pfam; PF00104; hormone_rec; 1.
CC DR Pfam; PF00105; zf-C4; 1.
CC DR PRINTS; PR00398; STRDHORMONER.
CC DR PRINTS; PR00047; STROIDFINGER.
CC DR PRODOM; PD000035; Znfc_Casteroid; 1.
CC DR SMART; SM00430; HOLI; 1.
CC DR SMART; SM00399; Znfc_C4; 1.
CC DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Phosphorylation.
CC FT DNA_BIND 24 89 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 24 44 C4-TYPE.
CC FT ZN_FING 50 84 C4-TYPE.
CC FT ZN_FING 90 187 HINGE.
CC FT DOMAIN 188 423 LIGAND-BINDING.
CC FT DOMAIN 423 423 LIGAND-BINDING.
CC SQ SEQUENCE 423 AA; 47813 MW; 1A0E519A9DCC990 CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 423;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLRPRKPMVTGSLPKKQPCDHPKGNVKKTRHQRHHRKPNKHSRACQQLK 108
| | | | | : | | | | | : | | | | | : | | | | |
Db 41 CEGCKGFFRRSMKRKALFT-----CP----FNGDCRITKDNR-----RHQACR--LK 82
| | | | | : | | | | | : | | | | | : | | | | |

QY 109 QC-----QLRSFAL 117
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Db 83 RCVDIGMKNKEFIL 95
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RESULT 15
VDR_BOVIN STANDARD; PRT; 424 AA.
AC Q28037;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin D3 receptor (VDR) (1,25-dihydroxyvitamin D3 receptor).
GN VDR OR NR111.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=97034797; PubMed=8880453;
RX Neibergs H.L., Bosworth B.T., Reinhardt T.A.;
RA "Nucleotide sequence of the bovine vitamin D3 receptor."
RL J. Dairy Sci. 79:1313-1315(1996).
CC -|- FUNCTION: Nuclear hormone receptor. VDR mediates the action of
CC vitamin D3 by controlling the expression of hormone sensitive
CC genes.
CC -|- SUBUNIT: Interacts with NCOA3 and NCOA6 coactivators, leading to a
CC strong increase of transcription of target genes (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear.
CC -|- DOMAIN: Composed of three domains: a modulating N-terminal domain,
CC a DNA-binding domain and a C-terminal steroid-binding domain.
CC -|- SIMILARITY: Belongs to the nuclear hormone receptor family. NR1
CC subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U50200; AAB01543.1; -.
CC HSSP; O75469; ILIG.
CC DR InterPro; IPR000536; Hormone_rec_lig.
CC DR InterPro; IPR001723; Stdhnm_receptor.
CC DR InterPro; IPR001628; Znfc_Casteroid.
CC DR Pfam; PF00104; hormone_rec; 1.
CC DR Pfam; PF00105; zf-C4; 1.
CC DR PRINTS; PR00398; STRDHORMONER.
CC DR PRINTS; PR00047; STROIDFINGER.
CC DR PRODOM; PD000035; Znfc_Casteroid; 1.
CC DR SMART; SM00430; HOLI; 1.
CC DR SMART; SM00399; Znfc_C4; 1.
CC DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger; Phosphorylation.
CC FT DNA_BIND 21 86 NUCLEAR RECEPTOR-TYPE.
CC FT ZN_FING 21 41 C4-TYPE.
CC FT ZN_FING 57 81 C4-TYPE.
CC FT ZN_FING 87 188 HINGE.
CC FT DOMAIN 189 424 LIGAND-BINDING.
CC FT DOMAIN 424 424 LIGAND-BINDING.
CC SQ SEQUENCE 424 AA; 47957 MW; E9E24926CE38CB7D CRC64;

Query Match 10.6%; Score 68.5; DB 1; Length 424;
Best Local Similarity 30.1%; Pred. No. 7.2;
Matches 22; Conservative 13; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLRPRKPMVTGSLPKKQPCDHPKGNVKKTRHQRHHRKPNKHSRACQQLK 108
| | | | | : | | | | | : | | | | | : | | | | |
Db 38 CEGCKGFFRRSMKRKALFT-----CP----FNGDCRITKDNR-----RHQACR--LK 79
| | | | | : | | | | | : | | | | | : | | | | |
```

OY 109 QC----QLRSPAL 117
: : : : :
Db 80 RCVDIGMKEFIL 92

Search completed: January 29, 2004, 11:54:51
Job time : 16 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: January 29, 2004, 11:52:48 ; Search time 20 Seconds
(without alignments)
572.204 Million cell updates/sec

Title: US-09-786-260-1
Perfect score: 644
Sequence: 1 MKVLISLLLLFLMLMSNV.....SRACQFLKQCLRSFALPL 119
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77.5	12.0	477	2	T18801
2	77	12.0	2269	1	JQ1750
3	74.5	11.6	448	2	I50451
4	73.5	11.4	70	2	A60912
5	71.5	11.1	108	2	G84522
6	71	11.0	411	2	S33333
7	71	11.0	2282	2	S16664
8	71	11.0	3190	2	T13828
9	70.5	10.9	1283	2	T49804
10	70	10.9	543	2	A34593
11	70	10.9	746	2	B32693
12	70	10.9	1095	2	T24061
13	70	10.9	1620	2	T27283
14	69.5	10.8	221	2	C34768
15	69.5	10.8	575	1	THUB
16	69	10.7	200	2	C83086
17	68.5	10.6	381	2	A46358
18	68.5	10.6	422	2	PC4019
19	68.5	10.6	423	2	A31761
20	68.5	10.6	427	2	A28200
21	68.5	10.6	427	2	S24174
22	68.5	10.6	647	2	S36557
23	68.5	10.6	1006	2	S74992
24	68	10.6	283	2	S42393
25	67	10.4	376	2	T48950
26	67	10.4	475	2	E68643
27	67	10.4	1062	2	T14151
28	67	10.4	1062	2	T30255
29	66.5	10.3	103	2	A72713

30 66.5 10.3 419 2 A57000 orphan receptor CO
31 66.5 10.3 422 2 I48305 gene COUP-TF1 prot
32 66.5 10.3 423 2 S02710 transcription fact
33 66 10.2 339 2 T36061 hypothetrical prote
34 65.5 10.2 106 2 S60232 gibberellin-regula
35 65.5 10.2 397 2 S26617 transcription fact
36 65.5 10.2 413 2 H82270 hypothetrical prote
37 65.5 10.2 425 2 JC7230 vitamin D receptor
38 65.5 10.2 646 2 S36586 E1 protein - human
39 65.5 10.2 706 2 JE0164 frizzled-6 protein
40 65 10.1 363 2 JC4748 polygalacturonase
41 65 10.1 440 2 JS0374 hypothetrical 51.6K
42 65 10.1 1797 2 A56677 laminin beta-2 cha
43 64.5 10.0 359 2 E29960 Balbiani ring 2 ch
44 64.5 10.0 622 2 I48733 protein kinase rck
45 64 9.9 227 2 I39313 zinc-finger protei

ALIGNMENTS

RESULT 1
T18801
hypothetical protein ZK131.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C:Accession: T18801; T27746
R:Percy, C.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19024
A:Accession: T18801
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-477 <WIL>
A:Cross-references: EMBL:Z93373; PIDN:CAB07552.1; GSPDB:GN00020; CESP:ZK131.11
A:Experimental source: clone C01B9
submitted to the EMBL Data Library, December 1996
A:Reference number: Z20413
A:Accession: T27746
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-477 <W12>
A:Cross-references: EMBL:Z83245; PIDN:CAB05840.1; GSPDB:GN00020; CESP:ZK131.11
A:Experimental source: clone ZK131
C:Genetics:
A:Gene: CESP:ZK131.11
A:Map position: 2
A:Introns: 20/2; 49/2; 113/1; 169/1; 260/2; 375/3; 432/3
C:Superfamily: Caenorhabditis elegans hypothetical protein ZK131.11

Query Match 12.0%; Score 77.5; DB 2; Length 477;
Best Local Similarity 34.7%; Pred. No. 2.3;
Matches 25; Conservative 6; Mismatches 32; Indels 9; Gaps 3;
QY 46 GQGECEKDWFLRAPRR---KFMVSLGPKQ--CPDHFKNVKKTRHQHHRKPKHS 100
Db 290 GGFNAESNTFLRATKRFKKIYTSATLPKKQNSMDNFKQSVFFEDTAHHHPNDG 349
QY 101 RACQFLKQCOL 112
Db 350 R-----ILKKAPL 357

RESULT 2
JQ1750
genome polyprotein - simian paramyxovirus SV41 (strain Toshiba/Chanock)
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: simian paramyxovirus SV41
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jun-1999
C:Accession: JQ1750
R:Ogawa, M.; Mutsuga, N.; Tsurudome, M.; Kawano, M.; Matsumura, H.; Kueagawa, S.; Komadi

J. Gen. Virol. 73, 2743-2750, 1992
A:Title: Nucleotide sequence analysis of the simian virus 41 gene encoding the large (L)
A:Reference number: JQ1750; MUID:93019033; PMID:1328465
A:Accession: JQ1750
A:Molecule type: mRNA
A:Residues: 1-2269 <OGA>
A:Cross-references: EMBL:X64275; NID:G433516; PIDN:CAA45569.1; PID:G433522
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase; RNA biosynthesis; RNA replication

Query Match 12.0%; Score 77; DB 1; Length 2269;
Best Local Similarity 27.5%; Pred. No. 10;
Matches 30; Conservative 12; Mismatches 31; Indels 36; Gaps 6;

QY 13 PLMLMSVSSSLNPGVARGHRDQAS-----RRWLQ-----EGQGECE--CK 53
DB 422 PLSLPGNASKSL-----TELHNDNSEISYEYTLRWKLSLIEFKKCFDFDPCGEELSIFMK 477

QY 54 DWFLRPRPRKFMVTGSLPKQPCDHFKNVKKTRHQRH-RKPNKHSR 101
DB 478 DKAISAPKEDWMSV-----FRSLIKQRHQRHIMPDPNFR 514

RESULT 3
150451
vitamin D receptor isoform A - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
A:Accession: I50451
R:Elaroussi, M.A.; Prah, J.M.; Deluca, H.F.
Proc. Natl. Acad. Sci. U.S.A. 91, 11596-11600, 1994
A:Title: The avian vitamin D receptors: primary structures and their origins.
A:Reference number: I50451; MUID:95062315; PMID:7972109
A:Accession: I50451
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-448 <ELA>
A:Cross-references: EMBL:U12641; NID:G95500; PIDN:AAA56725.1; PID:G95501
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:42-362/Domain: erba transforming protein homology <ERBA>

Query Match 11.6%; Score 74.5; DB 2; Length 448;
Best Local Similarity 32.9%; Pred. No. 4.5;
Matches 24; Conservative 11; Mismatches 15; Indels 23; Gaps 6;

QY 50 CE-CKDWFLRPRPRKFMVTGSLPKQPCDHFKNVKKTRHQRH-RKPNKHSRACQOFLK 108
DB 61 CEGCKGFFRRSKRKAMFT-----CP---FSGDCKITKDNR-----RHQOACR--LK 102

QY 109 QC-----QLRSFAL 117
DB 103 RCVDIGMKKEFL 115

RESULT 4
A60912
vitamin D receptor - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 12-Sep-1997
A:Accession: A60912
R:McDonnell, D.F.; Mangelsdorf, D.J.; Pike, J.W.; Hausler, M.R.; O'Malley, B.W.
Science 235, 1214-1217, 1987
A:Title: Molecular cloning of complementary DNA encoding the avian receptor for vitamin
A:Reference number: A60912; MUID:87149040; PMID:3029866
A:Accession: A60912
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-70 <MCD>
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; zinc finger

F:1-70/Domain: erba transforming protein homology (fragment) <ERBA>

Query Match 11.4%; Score 73.5; DB 2; Length 70;
Best Local Similarity 35.5%; Pred. No. 1.1;
Matches 22; Conservative 9; Mismatches 12; Indels 19; Gaps 5;

QY 50 CE-CKDWFLRPRPRKFMVTGSLPKQPCDHFKNVKKTRHQRH-RKPNKHSRACQOFLK 108
DB 20 CEGCKGFFRRSKRKAMFT-----CP---FNGDCKITKDNR-----RHQOACR--LK 61

QY 109 QC 110
DB 62 RC 63

RESULT 5
G84522
similar to gibberellin-regulated proteins [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
A:Accession: G84522
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, I.
ess, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <STO>
A:Cross-references: GB:AE002093; NID:G3650032; PIDN:AAC61287.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g14900
A:Map position: 2
C:Superfamily: gibberellin-regulated protein GAS2

Query Match 11.1%; Score 71.5; DB 2; Length 108;
Best Local Similarity 25.9%; Pred. No. 2.7;
Matches 29; Conservative 18; Mismatches 38; Indels 27; Gaps 7;

QY 1 MKVLISLLLL-LPLMLMSVSSSLNPGVARG-----HRDRGQASRWLQEGQGECE-- 51
DB 1 MKLIVSILVLASLLISSLASATISDAFGSAVAPAPQSKDGPALKWC---GQKCEGR 57

QY 52 CKDWFLRPRPRKFMVTGSLPKQPCDHFKNVKKTRHQRH-RKPNKHSRAC 103
DB 58 CKE---AGMKDRCLKYCGICCKDQC-----VPSGTY-----GNKHECAC 94

RESULT 6
S35333
steroid receptor protein svp44 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 24-Sep-1999
A:Accession: S35333
R:Pfjose, A.; Nornes, S.; Weber, U.; Mlodzik, M.
EMBO J. 12, 1403-1414, 1993
A:Title: Functional conservation of vertebrate seven-up related genes in neurogenesis a
A:Reference number: S35333; MUID:93223680; PMID:8467797
A:Accession: S35333
A:Molecule type: mRNA
A:Residues: 1-411 <FTO>
A:Cross-references: EMBL:X70299; NID:G296418; PIDN:CAA45780.1; PID:G296419
C:Genetics:
A:Gene: svp44
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; steroid hormone receptor; zinc finger
F:74-320/Domain: erba transforming protein homology <ERBA>
F:76-96/Region: zinc finger
F:112-136/Region: zinc finger

Query Match 11.0%; Score 71; DB 2; Length 411;

```

Db      2430 QHTNCKX--RKPNGGCPICKQLIALC 2453

RESULT 9
T49804
hypothetical protein B11B22.60 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49804
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49804
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1283 <SCH>
A:Cross-references: EMBL:AL358834; GSPDB:GNC0116; NCSP:B11B22.60
A:Experimental source: BAC clone B11B22; strain OR74A
C:Genetics:
A:Gene: NCSP:B11B22.60
A:Map position: 6
A:Introns: 856/2

Query Match      10.9%; Score 70.5; DB 2; Length 1283;
Best Local Similarity 24.5%; Pred. No. 29;
Matches 26; Conservative 18; Mismatches 31; Indels 31; Gaps 6;

QY      33 RDRQASRWLQGGGCECKWFLAPRKWTYS--GLPKQCPDHFKNVKK--T 87
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          454 RNKNKKQKQKQSGKSGK-----LRAPESAMPPVSVWVGSPRAWPLRWQGHIRNGDV 508
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          QY      88 RHQRHR-----KPNKHSRACQF--LKQCQLRSPA 116
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          DB      509 QHOSHQMYWDEGYVRLWSEKLEPH---QQFARLRKAELALYA 550
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
A32693
steroid receptor protein svp 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C:Accession: A32693
R:Midzik, M.; Hifromi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A:Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily
A:Reference number: A32693; MUID:90124631; PMID:2105166
A:Accession: A32693
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-543 <MLO>
A:Cross-references: GB:M28863; NID:g158518; PIDN:AAA62770.1; PID:g158519
C:Genetics:
A:Gene: FlyBase:svp
A:Cross-references: FlyBase:FBgn0003651
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription;
F:198-452/Domain: erba transforming protein homology <ERBA>
F:200-220/Region: zinc finger
F:236-260/Region: zinc finger

Query Match      10.9%; Score 70; DB 2; Length 543;
Best Local Similarity 26.7%; Pred. No. 16;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY      21 SSSINPG-----VARGHRDQGSARWLQGGGCECKQWFLAPRKWTVSG 69
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          DB      183 SQSSNSGSDSKQNTIECVVCGDKSGKHVQGTCEG-----CKSFFKRSVRN-LTYS 236
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          QY      70 LPKKQCPDHFKNVKKTRHHRKPKHSRACQFLKQC 110
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          DB      237 RGSRNCPID-----QHRNQCCQICR-----LKKC 260
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
RESULT 11
B32693
steroid receptor protein svp 2 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 12-Sep-1997
C/Accession: B32693
R:Modzik, M.; Hiroimi, Y.; Weber, U.; Goodman, C.S.; Rubin, G.M.
Cell 60, 211-224, 1990
A>Title: The Drosophila seven-up gene, a member of the steroid receptor gene superfamily
A/Reference number: A32693; MUID:90124631; PMID:2105166
A/Accession: B32693
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-746 <MLO>
A/Cross-references: GB:M28863; GB:M28864
C/Genetics:
A/Gene: FlyBase:svp
A/Cross-references: FlyBase:FBgn0003651
C/Superfamily: unassigned erba-related proteins; erba transforming protein homology
C/Keywords: alternative splicing; DNA binding; steroid hormone receptor; transcription
F:198-452/Dominant: erba transforming protein homology <ERBA>
F:200-220/Region: zinc finger
F:236-260/Region: zinc finger

Query Match 10.9%; Score 70; DB 2; Length 746;
Best Local Similarity 26.7%; Pred. No. 21;
Matches 27; Conservative 12; Mismatches 28; Indels 34; Gaps 5;

QY 21 SSSLNPG-----VARGHRDQASRWLQEGQCECKDWFLRAPRRKFTMTVSG 69
DB 183 SOSNSGSGQIDSKQNIQVCGDKSSGKHVQFTCEG-----CKSPFKGSVRN-LTYS 236
QY 70 LFKKQCPDHFPGNVKTRHORHRKPKHKSRAQQFLKQC 110
DB 237 RGRNCPID-----QHRNQCYCR-----LKKC 260

RESULT 12
T24061
hypothetical protein R09A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C/Accession: T24061
R:Wilkinson, J.
A/Reference number: Z19836
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1095 <WIL>
A/Cross-references: EMBL:Z68009; PIDN:CAA92003.1; GSPDB:GN00028; CESP:R09A8.1
A/Experimental source: clone R09A8
C/Genetics:
A/Gene: CESP:R09A8.1
A/Map position: X
A/Introns: 48/2; 189/1; 285/3; 347/3; 402/3; 482/3; 543/3; 619/1; 693/1; 771/1; 835/1; 1

Query Match 10.9%; Score 70; DB 2; Length 1095;
Best Local Similarity 31.6%; Pred. No. 29;
Matches 24; Conservative 10; Mismatches 32; Indels 10; Gaps 3;

QY 20 VSSSLNPGVARGHRDQASRWLQEGQCECKDWFLRAPRRKFTMTVSGLPKKQCFCH 79
DB 305 VSSSLMVGNGRTDVRVNA-QRFASGTFVECKRRDQLVEKKQ-----KKEVNSDH 355
QY 80 FKGNVKKTRHQRRHK 95
DB 356 KKAN-RITSHLEHNSR 370

RESULT 13
T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T27283
R:Ainscough, R.
A/Reference number: Z20336
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1620 <WIL>
A/Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f
A/Experimental source: clone Y64G10A
C/Genetics:
A/Gene: CESP:Y64G10A.f
A/Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 695/1;

Query Match 10.9%; Score 70; DB 2; Length 1620;
Best Local Similarity 30.0%; Pred. No. 40;
Matches 21; Conservative 10; Mismatches 35; Indels 4; Gaps 3;

QY 46 GQGECECKDWFLRAPRRKFTMTVSGLPKKQCPDHFPGNVKTRH--QRHHRKPKHKSRA 102
DB 261 GRAQCQCYPGFHLSYDRRSCVDIDCAKNN-GCEHFCENVKGTCKREGYQLGRDGR 319
QY 103 COQFLKQCQL 112
DB 320 CEMLGGCQV 329

RESULT 14
C34768
ORF2 protein - Orf virus (strain NZ2)
C:Species: Orf virus
C>Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Oct-1999
C/Accession: C34768
R:Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A>Title: Sequence analysis of the inverted terminal repetition in the genome of the par
A/Reference number: A34768; MUID:90266454; PMID:2129563
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-221 <FRA>
A/Cross-references: GB:M30023; EMBL:M37623; NID:G332561; PIDN:AAA46789.1; PID:G332565

Query Match 10.8%; Score 69.5; DB 2; Length 221;
Best Local Similarity 29.2%; Pred. No. 8.1;
Matches 33; Conservative 8; Mismatches 37; Indels 35; Gaps 6;

QY 26 PGVARGHRDQASRWLQEGQCECKDWFLRAPRRKFTMTVSGLPKK-----QCP 76
DB 83 PAARAGARRRGCCARRARGGGWF---RWRPFAARRG---SGPPAPAPAAALAPDQAP 135
QY 77 CDHFKNVKKTR-----HOR--HHRKPKHKSRAQQFLKQCQLRS 114
DB 136 ----RSVKVKORLAVETLPQPTPTHTLPPARRQHRSSQACTPRRAGCSARS 184

RESULT 15
THHUB
thrombomodulin precursor [validated] - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1988 #sequence_revision 12-May-1995 #text_change 15-Sep-2000
C/Accession: A41442; A28307; A29680; A27073; JX0264; S39554
R:Shirai, T.; Shiojiri, S.; Ito, H.; Yamamoto, S.; Kusumoto, H.; Deyashiki, Y.; Maruyama, J. Biochem. 103, 281-285, 1988
A>Title: Gene structure of human thrombomodulin, a cofactor for thrombin-catalyzed acti
A/Reference number: A41442; MUID:88227901; PMID:2836377
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-575 <SHI>
A/Cross-references: DBJ:D00210; NID:G220126; PIDN:BAA00149.1; PID:G220127
R:Jackman, R.W.; Beeler, D.L.; Fritze, G.; Rosenberg, R.D.
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Proc. Natl. Acad. Sci. U.S.A. 84, 6425-6429, 1987
 A:Title: Human thrombomodulin gene is intron depleted: nucleic acid sequences of the cDN
 A:Reference number: A28307; MUID:87317665; PMID:2819876
 A:Accession: A28307
 A:Molecule type: DNA; mRNA
 A:Residues: 1-472, 'A', 474-575 <JAC>
 A:Cross-references: GB:J02973; NID:G339658; PIDN:AAA61175.1; PID:G339659
 R:Suzuki, K.; Kusumoto, H.; Deyashiki, Y.; Nishioka, J.; Maruyama, I.; Zushi, M.; Kawaha
 EMBO J. 6, 1891-1897, 1987
 A:Title: Structure and expression of human thrombomodulin, a thrombin receptor on endoth
 A:Reference number: A29680; MUID:88004395; PMID:2820710
 A:Accession: A29680
 A:Molecule type: mRNA
 A:Residues: 1-575 <SUZ>
 A:Cross-references: GB:X05495; NID:G37123; PIDN:CAA29045.1; PID:G736251
 A:Experimental source: lung endothelium
 A:Note: part of this sequence, including the amino end of the mature protein, were deter
 R:Wen, D.; Dittman, W.A.; Ye, R.D.; Deaven, L.L.; Majerus, P.W.; Sadler, J.E.
 Biochemistry 26, 4350-4357, 1987
 A:Title: Human thrombomodulin: complete cDNA sequence and chromosome localization of the
 A:Reference number: A27073; MUID:88024950; PMID:2822087
 A:Accession: A27073
 A:Molecule type: mRNA
 A:Residues: 1-472, 'A', 474-575 <WEN>
 A:Cross-references: GB:M16552; NID:G339656; PIDN:AAB59508.1; PID:G339657
 A:Experimental source: placenta
 A:Note: parts of this sequence were determined by protein sequencing
 R:Yamamoto, S.; Mizoguchi, T.; Tamaki, T.; Ohkuchi, M.; Kimura, S.; Aoki, N.
 J. Biochem. 113, 433-440, 1993
 A:Title: Urinary thrombomodulin, its isolation and characterization.
 A:Reference number: JX0264; MUID:93293792; PMID:8390446
 A:Accession: JX0264
 A:Molecule type: protein; mRNA
 A:Residues: 19-472, 'A', 474-486 <YAM>
 A:Experimental source: urine
 A:Note: the urinary form appears to be identical with that circulating in plasma
 R:Garlitz, B.; Hassell, T.; Vlahos, C.J.; Parkinson, J.F.; Bang, N.U.; Grinnell, B.W.
 Biochem. J. 295, 131-140, 1993
 A:Title: Identification of the predominant glycosaminoglycan-attachment site in soluble
 serine.
 A:Reference number: S38954; MUID:94029900; PMID:8216207
 A:Accession: S38954
 A:Molecule type: protein
 A:Residues: 475-491, 'X', 493-494 <GER>
 A:Note: the residue designated 'X' was determined to be a Ser with covalently bound chon
 R:Meininger, D.P.; Komives, E.A.
 submitted to the Brookhaven Protein Data Bank, September 1995
 A:Reference number: A67369; PDB:1ZQA
 A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 R:Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, August 1994
 A:Reference number: A52804; PDB:1HLT
 A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 426-442
 R:Hrabal, R.; Komives, E.A.; Ni, F.
 submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A65583; PDB:1FGD
 A:Contents: annotation; conformation by (1)H-NMR, residues 427-444
 R:Hrabal, R.; Komives, E.A.; Ni, F.
 Protein Sci. 5, 195-203, 1996
 A:Title: Structural resiliency of an EGF-like subdomain bound to its target protein, thr
 A:Reference number: A58595; MUID:96276211; PMID:8745396
 A:Contents: annotation; conformation by (1)H-NMR
 C:Genetics:
 A:Gene: GDB:THBD
 A:Cross-references: GDB:119613; OMIM:188040
 A:Map position: 20p11.2-20p11.2
 A:Introns: #status absent
 C:Complex: homodimer, urinary form
 C:Function:
 A:Description: inhibits thrombin activation of fibrinogen; cofactor for thrombin activat
 A:Pathway: blood coagulation moderation
 A:Note: the membrane-bound form is located on the endothelium luminal surface of arterie
 A:Note: thrombin complexed with the membrane-bound form is subject to endocytosis

C:Superfamily: thrombomodulin; C-type lectin homology; EGF homology
 C:Keywords: anticoagulant; beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coa
 e protein
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-575/Product: thrombomodulin, membrane-bound form #status predicted <MAT>
 F:19-513/Domain: extracellular #status predicted <EXT>
 F:19-486/Product: thrombomodulin, urinary form #status experimental <MAU>
 F:24-167/Domain: C-type lectin homology <LCH>
 F:177-199/Region: PEST sequence
 F:201-233/Region: PEST sequence
 F:245-280/Domain: EGF homology <EG1>
 F:288-323/Domain: EGF homology <EG2>
 F:329-362/Domain: EGF homology <EG3>
 F:369-404/Domain: EGF homology <EG4>
 F:408-439/Domain: EGF homology <EG5>
 F:445-480/Domain: EGF homology <EG6>
 F:485-513/Region: PEST sequence
 F:517-539/Domain: transmembrane #status predicted <TMN>
 F:540-575/Domain: intracellular #status predicted <INT>
 F:174,225,411,504/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:174,225,411,504/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F:245-256,252-265,267-280,288-296,292-308,310-323,329-340,336-349,351-362,369-378,374-3
 F:334,498/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:342/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
 F:490,492/Binding site: chondroitin sulfate (Ser) (covalent) (partial) #status experimer
 Query Match 10.8%; Score 69.5; DB 1; Length 575;
 Best Local Similarity 23.5%; Pred. No. 18;
 Matches 24; Conservative 11; Mismatches 26; Indels 41; Gaps 5;
 QY 5 ISSLLILLPLMLMSVSSLNPVGVARHRRDQASRRW---LQEGGQCECKQWFLRAPR 61
 Db 209 VGSSAAVAPLGLQLMCTAP--FGAVQGHWR-EAPGAWDCSVENGCGEACN----- 257
 QY 62 RKFMVSVGLPKKQCP-----CDHF 80
 Db 258 ----AIPGAPRCQCPAGALQADGRSCTASATQSCNDLCEHF 295
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